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Pro Phe Lys Cys Thr Tyr Cys Ser Arg Leu Phe Lys His Lys Arg Ser
145                 150                 155                 160
Arg Asp Arg His Ile Lys Leu His Thr Gly Asp Lys Lys Tyr His Cys
                165                 170                 175
Ser Glu Cys Asp Ala Ala Phe Ser Arg Ser Asp His Leu Lys Ile His
            180                 185                 190
Leu Lys Thr His Thr Ser Asn Lys Pro Tyr Lys Cys Ala Ile Cys Arg
        195                 200                 205
Arg Gly Phe Leu Ser Ser Ser Ser Leu His Gly His Met Gln Val His
    210                 215                 220
Glu Arg Asn Lys Asp Gly Ser Gln Ser Gly Ser Arg Met Glu Asp Trp
225                 230                 235                 240
Lys Met Lys Asp Thr Gln Lys Cys Ser Gln Cys Glu Glu Gly Phe Asp
                245                 250                 255
Phe Pro Glu Asp Leu Gln Lys His Ile Ala Glu Cys His Pro Glu Cys
            260                 265                 270
Ser Pro Asn Glu Asp Arg Ala Ala Leu Gln Cys Val Tyr Cys His Glu
        275                 280                 285
Leu Phe Val Glu Glu Thr Ser Leu Met Asn His Met Glu Gln Val His
    290                 295                 300
Ser Gly Glu Lys Lys Asn Ser Cys Ser Ile Cys Ser Glu Ser Phe His
305                 310                 315                 320
Thr Val Glu Glu Leu Tyr Ser His Met Asp Ser His Gln Gln Pro Glu
                325                 330                 335
Ser Cys Asn His Ser Asn Ser Pro Ser Leu Val Thr Val Gly Tyr Thr
            340                 345                 350
Ser Val Ser Ser Thr Thr Pro Asp Ser Asn Leu Ser Val Asp Ser Ser
        355                 360                 365
Thr Met Val Glu Ala Ala Pro Pro Ile Pro Lys Ser Arg Gly Arg Lys
    370                 375                 380
Arg Ala Ala Gln Gln Thr Pro Asp Met Thr Gly Pro Ser Ser Lys Gln
385                 390                 395                 400
Ala Lys Val Thr Tyr Ser Cys Ile Tyr Cys Asn Lys Gln Leu Phe Ser
                405                 410                 415
Ser Leu Ala Val Leu Gln Ile His Leu Lys Thr Met His Leu Asp Lys
            420                 425                 430
Pro Glu Gln Ala His Ile Cys Gln Tyr Cys Leu Glu Val Leu Pro Ser
        435                 440                 445
Leu Tyr Asn Leu Asn Glu His Leu Lys Gln Val His Glu Ala Gln Asp
    450                 455                 460
Pro Gly Leu Ile Val Ser Ala Met Pro Ala Ile Val Tyr Gln Cys Asn
465                 470                 475                 480
Phe Cys Ser Glu Val Val Asn Asp Leu Asn Thr Leu Gln Glu His Ile
                485                 490                 495
Arg Cys Ser His Gly Phe Ala Asn Pro Ala Ala Lys Asp Ser Asn Ala
            500                 505                 510
Phe Phe Cys Pro His Cys Tyr Met Gly Phe Leu Thr Asp Ser Ser Leu
        515                 520                 525
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Glu Glu His Ile Arg Gln Val His Cys Asp Leu Ser Gly Ser Arg Phe
530 535 540
Gly Ser Pro Val Leu Gly Thr Pro Lys Glu Pro Val Val Glu Val Tyr
545 550 555 560
Ser Cys Ser Tyr Cys Thr Asn Ser Pro Ile Phe Asn Ser Val Leu Lys
565 570 575
Leu Asn Lys His Ile Lys Glu Asn His Lys Asn Ile Pro Leu Ala Leu
580 585 590
Asn Tyr Ile His Asn Gly Lys Lys Ser Arg Ala Leu Ser Pro Leu Ser
595 600 605
Pro Val Ala Ile Glu Gln Thr Ser Leu Lys Met Met Gln Ala Val Gly
610 615 620
Gly Ala Pro Ala Arg Pro Thr Gly Glu Tyr Ile Cys Asn Gln Cys Gly
625 630 635 640
Ala Lys Tyr Thr Ser Leu Asp Ser Phe Gln Thr His Leu Lys Thr His
645 650 655
Leu Asp Thr Val Leu Pro Lys Leu Thr Cys Pro Gln Cys Asn Lys Glu
660 665 670
Phe Pro Asn Gln Glu Ser Leu Leu Lys His Val Thr Ile His Phe Met
675 680 685
Ile Thr Ser Thr Tyr Tyr Ile Cys Glu Ser Cys Asp Lys Gln Phe Thr
690 695 700
Ser Val Asp Asp Leu Gln Lys His Leu Leu Asp Met His Thr Phe Val
705 710 715 720
Phe Phe Arg Cys Thr Leu Cys Gln Glu Val Phe Asp Ser Lys Val Ser
725 730 735
Ile Gln Leu His Leu Ala Val Lys His Ser Asn Glu Lys Lys Val Tyr
740 745 750
Arg Cys Thr Ser Cys Asn Trp Asp Phe Arg Asn Glu Thr Asp Leu Gln
755 760 765
Leu His Val Lys His Asn His Leu Glu Asn Gln Gly Lys Val His Lys
770 775 780
Cys Ile Phe Cys Gly Glu Ser Phe Gly Thr Glu Val Glu Leu Gln Cys
785 790 795 800
His Ile Thr Thr His Ser Lys Lys Tyr Asn Cys Lys Phe Cys Ser Lys
805 810 815
Ala Phe His Ala Ile Ile Leu Leu Glu Lys His Leu Arg Glu Lys His
820 825 830
Cys Val Phe Glu Thr Lys Thr Pro Asn Cys Gly Thr Asn Gly Ala Ser
835 840 845
Glu Gln Val Gln Lys Glu Glu Val Glu Leu Gln Thr Leu Leu Thr Asn
850 855 860
Ser Gln Glu Ser His Asn Ser His Asp Gly Ser Glu Glu Asp Val Asp
865 870 875 880
Thr Ser Glu Pro Met Tyr Gly Cys Asp Ile Cys Gly Ala Ala Tyr Thr
885 890 895
Met Glu Thr Leu Leu Gln Asn His Gln Leu Arg Asp His Asn Ile Arg
900 905 910

Pro Gly Glu Ser Ala Ile Val Lys Lys Lys Ala Glu Leu Ile Lys Gly
915 920 925
Asn Tyr Lys Cys Asn Val Cys Ser Arg Thr Phe Phe Ser Glu Asn Gly
930 935 940
Leu Arg Glu His Met Gln Thr His Leu Gly Pro Val Lys His Tyr Met
945 950 955 960
Cys Pro Ile Cys Gly Glu Arg Phe Pro Ser Leu Leu Thr Leu Thr Glu
965 970 975
His Lys Val Thr His Ser Lys Ser Leu Asp Thr Gly Asn Cys Arg Ile
980 985 990
Cys Lys Met Pro Leu Gln Ser Glu Glu Glu Phe Leu Glu His Cys Gln
995 1000 1005
Met His Pro Asp Leu Arg Asn Ser Leu Thr Gly Phe Arg Cys Val Val
1010 1015 1020
Cys Met Gln Thr Val Thr Ser Thr Leu Glu Leu Lys Ile His Gly Thr
1025 1030 1035 1040
Phe His Met Gln Lys Thr Gly Asn Gly Ser Ala Val Gln Thr Thr Gly
1045 1050 1055
Arg Gly Gln His Val Gln Lys Leu Tyr Lys Cys Ala Ser Cys Leu Lys
1060 1065 1070
Glu Phe Arg Ser Lys Gln Asp Leu Val Lys Leu Asp Ile Asn Gly Leu
1075 1080 1085
Pro Tyr Gly Leu Cys Ala Gly Cys Val Asn Leu Ser Lys Ser Ala Ser
1090 1095 1100
Pro Gly Ile Asn Val Pro Pro Gly Thr Asn Arg Pro Gly Leu Gly Gln
1105 1110 1115 1120
Asn Glu Asn Leu Ser Ala Ile Glu Gly Lys Gly Lys Val Gly Gly Leu
1125 1130 1135
Lys Thr Arg Cys Ser Ser Cys Asn Val Lys Phe Glu Ser Glu Ser Glu
1140 1145 1150
Leu Gln Asn His Ile Gln Thr Ile His Arg Glu Leu Val Pro Asp Ser
1155 1160 1165
Asn Ser Thr Gln Leu Lys Thr Pro Gln Val Ser Pro Met Pro Arg Ile
1170 1175 1180
Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr Tyr Gln Cys Ile Lys Cys
1185 1190 1195 1200
Gln Met Val Phe Tyr Asn Glu Trp Asp Ile Gln Val His Val Ala Asn
1205 1210 1215
His Met Ile Asp Glu Gly Leu Asn His Glu Cys Lys Leu Cys Ser Gln
1220 1225 1230
Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys His Leu Ile Glu His Ser
1235 1240 1245
Phe Glu Gly Met Gly Gly Thr Phe Lys Cys Pro Val Cys Phe Thr Val
1250 1255 1260
Phe Val Gln Ala Asn Lys Leu Gln Gln His Ile Phe Ser Ala His Gly
1265 1270 1275 1280
Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln Cys Pr Gln Lys Phe Phe
1285 1290 1295

Phe Gln Thr Glu Leu Gln Asn His Thr Met Thr Gln His Ser Ser
1300 1305 1310

<210> 28
<211> 1988
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (160)..(876)

<400> 28
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ccaggaagtt cagagagaac agaatttaag aagtgcaaca tggccagggg ctgcctctgc 180
tgcttgaagt acatgatgtt cctcttcaat ttgatattct ggctctgtgg ctgtgggctg 240
ctgggagtgg gcatctggct ctccgtgtcc caaggcaact ttgccacctt ctcccccagc 300
ttcccttcgt tgtctgcagc caacctggtc attgccatag gcaccattgt catggtgacg 360
ggcttcctcg gctgcctggg ggccatcaag gaaaacaagt gcctcctcct cagcttttc 420
atcgtcctgt tggtcatcct cctagcagag ctgatcttac tcatcctctt ctttgtctac 480
atggacaagg tgaacgagaa cgccaagaag gacctgaagg aaggcctgct gctgtaccac 540
accgagaaca acgtggggct gaagaacgcc tggaacatca tccaggctga gatgcgatgc 600
tgtggtgtca ctgactacac agactggtac ccagtgctgg gggagaacac ggttcccgac 660
cgctgctgca tggagaactc ccagggctgc gggcgcaacg ccaccacgcc tttgtggaga 720
acgggctgct atgaaaaggt gaagatgtgg ttcgatgaca ataagcacgt gctgggcacg 780
gtggggatgt gcatcctcat catgcagatc ctgggcatgg ccttctccat gaccctcttc 840
cagcacatcc accggactgg taagaagtac gacgcatgag cgggctggcc gggagtgccc 900
accccgccct gctgccctgt ggagggaaga ggattgagct ttgtgtcacc tgcctgcgct 960
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cagcctcaga cttctcagtg ggtggagtgc cagggaggag gaggcacacg gagacctggg 1080
gctcggggcc cctggattcc tgcatctgca tgtgcgtatt tgccaaagac gacagggtgg 1140
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acactgacac tttgtcccca catggggtgg ggagcagagt gcccgccccg tggagatacc 1260
gccccagcgg gggctgcgac atctatggcc accatggggc acctggcggg gcgggggtct 1320
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aacttttta ttttatttta ctctatgatt attcaggaat attatctctc agataagttt 1440
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ttttccctga gggtgaggga tgggtgggaa gagaggacat ctgtcccctc ctctccagcc 1560
cctgcccacc cactggtgga ggtgctaact agcagggacg tggcatagga tgggagctgg 1620
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ccctccttgc ccacctgcct gcccccgggc agcacgggag ggagagcagg gtgagcacgc 1860
ttgttggttt cagatgcact ttctgcttgc attgccgtat ctgtgcgttc cttcatcctg 1920
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tcaaaagc 1988

<210> 29
<211> 239
<212> PRT
<213> Homo sapiens

<400> 29
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Asn Leu Ile Phe Trp Leu Cys Gly Cys Gly Leu Leu Gly Val Gly Ile
20 25 30
Trp Leu Ser Val Ser Gln Gly Asn Phe Ala Thr Phe Ser Pro Ser Phe
35 40 45
Pro Ser Leu Ser Ala Ala Asn Leu Val Ile Ala Ile Gly Thr Ile Val
50 55 60
Met Val Thr Gly Phe Leu Gly Cys Leu Gly Ala Ile Lys Glu Asn Lys
65 70 75 80
Cys Leu Leu Leu Ser Phe Phe Ile Val Leu Leu Val Ile Leu Leu Ala
85 90 95
Glu Leu Ile Leu Leu Ile Leu Phe Phe Val Tyr Met Asp Lys Val Asn
100 105 110
Glu Asn Ala Lys Lys Asp Leu Lys Glu Gly Leu Leu Leu Tyr His Thr
115 120 125
Glu Asn Asn Val Gly Leu Lys Asn Ala Trp Asn Ile Ile Gln Ala Glu
130 135 140
Met Arg Cys Cys Gly Val Thr Asp Tyr Thr Asp Trp Tyr Pro Val Leu
145 150 155 160
Gly Glu Asn Thr Val Pro Asp Arg Cys Cys Met Glu Asn Ser Gln Gly
165 170 175
Cys Gly Arg Asn Ala Thr Thr Pro Leu Trp Arg Thr Gly Cys Tyr Glu
180 185 190
Lys Val Lys Met Trp Phe Asp Asp Asn Lys His Val Leu Gly Thr Val
195 200 205
Gly Met Cys Ile Leu Ile Met Gln Ile Leu Gly Met Ala Phe Ser Met
210 215 220
Thr Leu Phe Gln His Ile His Arg Thr Gly Lys Lys Tyr Asp Ala
225 230 235

<210> 30
<211> 1900
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (128)..(1195)

<400> 30
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ccagtccatg ggttcttatg gacctttcgg caggatgccc acatacagtc agttcagtcc 180
gagttcctta gttgggcagc agtttggtgc tgttggtgtt gctggaagct ctttgacatc 240
ctttggaaca gaaacatcaa acagtggtac cttaccccaa agtagtgcgg ttggttctgc 300
ctttacacag gatacaagat ctctaaaaac acagttatct caaggtcgct caagccctca 360
gttagaccct ttgagaaaaa gcccaaccat ggaacaagca gtgcagaccg cctcagccca 420
cttacctgct ccagcagctg ttgggagaag gagtcctgta tcaaccaggc ctttgccatc 480
tgccagccaa aaggcaggag agaatcagga gcacaggcga gctgaagtac acaaagtttc 540
aaggccagaa aatgagcaac tcagaaatga taacaagaga caagtagctc caggtgctcc 600
ttcagctcca aggagagggc gtgggggtca tcggggtggc aggggaagat ttggtattcg 660
gcgagatggg ccaatgaaat ttgagaaaga ctttgacttt gaaagtgcaa atgcacaatt 720
caacaaggaa gagattgaca gagagtttca taataaactt aaattaaaag aagataaact 780
tgagaaacag gagaagcctg taaatggtga agataaagga gactcaggag ttgataccca 840
aaacagtgaa ggaaatgccg atgaagaaga tccacttgga cctaattgct attatgacaa 900
aactaaatcc ttctttgata atatttcttg tgatgacaat agagaacgga gaccaacctg 960
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tggcagaggt ggtaccttca ctgcccctcg aggatttcgc ggtggattca gaggaggtcg 1140
tgggggccgg gagtttgcgg attttgaata taggaaagac aacaaagttg ctgcatagtc 1200
tacaaacaag tctctgaaaa taggtgaatt tctagctctt catggtcctg aacattgatt 1260
tcagtctttg caaagaatga agaagtgaat tcgctgtaca tttgtcacca gcactgggtt 1320
tttgtttttt gtttgttttt ccgcttaatt tcaaagataa aatgcagtta cttttggggg 1380
tggaaggctc atcttaaaac atgagcatta aatatatttg gaatagcaga aggttaagta 1440
atttcttatg tatagttaaa ctaaagcagt acttcagtgg gacttaacaa gtatttttc 1500
atcactgaaa ggtttttttt ttttatcact aaattgtatt tggcaattgc aagttgcctg 1560
cagatagggc cgtgatactg tgttttgagc cacagaaggt tgtgtgtgtg tgtgtgtgtg 1620
tgtgtgtgtg tgtgtgtgta tgtgtgtgtc tttttcctcc tttcttttgg ggaatcctgt 1680
aatatgaggt agcttatttc gtcaattaat tagggtgctg gatggtagag aattttgtca 1740
gtcaactatg tacacacagt aaatactgtt tcttaggcaa aggtaacttt tttatatagt 1800
tgtaaaattc cattatattc cattgccaaa gaaacattaa gaactttgta tagctgtata 1860
aaaagcaact aatttttaa agaataaaca ttttaaagtc 1900

<210> 31
<211> 356
<212> PRT
<213> Homo sapiens

<400> 31
Met Gly Ser Tyr Gly Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe
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Ser Pro Ser Ser Leu Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala
20 25 30
Gly Ser Ser Leu Thr Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr
35 40 45

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Leu Pro Gln Ser Ser Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg
     50                  55                  60
Ser Leu Lys Thr Gln Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp
 65                  70                  75                  80
Pro Leu Arg Lys Ser Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser
                 85                  90                  95
Ala His Leu Pro Ala Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser
            100                 105                 110
Thr Arg Pro Leu Pro Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu
        115                 120                 125
His Arg Arg Ala Glu Val His Lys Val Ser Arg Pro Glu Asn Glu Gln
    130                 135                 140
Leu Arg Asn Asp Asn Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala
145                 150                 155                 160
Pro Arg Arg Gly Arg Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly
                165                 170                 175
Ile Arg Arg Asp Gly Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu
            180                 185                 190
Ser Ala Asn Ala Gln Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His
        195                 200                 205
Asn Lys Leu Lys Leu Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro
    210                 215                 220
Val Asn Gly Glu Asp Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser
225                 230                 235                 240
Glu Gly Asn Ala Asp Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr
                245                 250                 255
Asp Lys Thr Lys Ser Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg
            260                 265                 270
Glu Arg Arg Pro Thr Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr
        275                 280                 285
Phe Gly Ile Pro Leu Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly
    290                 295                 300
Arg Gly Gly Leu Gly Phe Arg Gly Gly Arg Gly Arg Gly Gly Gly Arg
305                 310                 315                 320
Gly Gly Thr Phe Thr Ala Pro Arg Gly Phe Arg Gly Gly Phe Arg Gly
                325                 330                 335
Gly Arg Gly Gly Arg Glu Phe Ala Asp Phe Glu Tyr Arg Lys Asp Asn
            340                 345                 350
Lys Val Ala Ala
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<210> 32
<211> 1877
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (127)..(840)

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gaggtgatga gcctcaacga gcactccatg caggcgctgt cctggcgcaa gctctacttg 180
agccgcgcca agcttaaagc ctccagccgg acctcggctc tgctctccgg cttcgccatg 240
gtggcaatgg tggaggtgca gctggacgct gaccacgact acccaccggg gctgctcatc 300
gccttcagtg cctgcaccac agtgctggtg gctgtgcacc tgtttgcgct catgatcagc 360
acctgcatcc tgcccaacat cgaggcggtg agcaacgtgc acaatctcaa ctcggtcaag 420
gagtcccccc atgagcgcat gcaccgccac atcgagctgg cctgggcctt ctccaccgtc 480
atcggcacgc tgctcttcct agctgaggtg gtgctgctct gctgggtcaa gttcttgccc 540
ctcaagaagc agccaggcca gccaaggccc accagcaagc cccccgccgg tggcgcagca 600
gccaacgtca gcaccagcgg catcaccccg ggccaggcag ccgccatcgc ctcgaccacc 660
atcatggtgc ccttcggcct gatctttatc gtcttcgcct tccacttcta ccgctcactg 720
gtcagccata agaccgaccg acagttccag gagctcaacg agctggcgga gtttgcccgc 780
ttacaggacc agctggacca cagaggggac caccccctga cgcccggcag ccactatgcc 840
taggcccatg tggtctgggc ccttccagtg ctttggcctt acgcccttcc ccatgacctt 900
gtcctgcccc agcctcacgg acagcctgtg caggggctg ggcttcagca aggggcagag 960
cgtggaggga agaggatttt tataagagaa atttctgcac tttgaaactg tcctctaaga 1020
gaataagcat ttcctgttct cccagctcca ggtccacctc ctgctgggag gcggtggggg 1080
gccaaagtgg ggccacacac tcgctgtgtc ccctctcctc ccctgtgcca gtgccacctg 1140
ggtgcctcct cctgtcctgt ccgtctcaac ctccctcccg tccagcattg agtgtgtaca 1200
tgtgtgtgtg acacataaat atactcataa ggacacctcc ttcccgtgtc ttgtatttgt 1260
tgggcctggg ctactgctca ccctggttag gtgagcctct aggaaaactt aaaacgaatt 1320
ttaagccagg tatggtggca catacctgtg gtctcagcta ttcaggaggc caaggcagga 1380
ggatctcttg agcccaggag tttgagaccc catctcaaac aaaaaataca aaaattagcc 1440
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gagggagact ctgtctctaa aaaaatagaa aaatttgccc tgcatggtgg ctcacgcctg 1620
taatcctagc cctttggaag gccaaggcgg gcagatcact tgaggtcggg agttcgagac 1680
cagcctgacc aacatggaga aaccccatct gtactaaaaa tacaaaatta gctgggtttg 1740
gtggcgcatg cttgtaatcc cagctactcg ggaggctgag gcaggagaat cgcttgaacc 1800
caggaggcgg aggttgcagt gagctgagat cgcgccattg cactccagcc tgggcaacaa 1860
cagtgaaact ccgtctc 1877

<210> 33
<211> 238
<212> PRT
<213> Homo sapiens

<400> 33
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Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
20 25 30

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Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
          35                  40                  45
Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr
      50                  55                  60
Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
 65                  70                  75                  80
Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
                 85                  90                  95
Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
            100                 105                 110
Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
        115                 120                 125
Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
    130                 135                 140
Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Gly Gly Ala Ala Ala Asn
145                 150                 155                 160
Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
                165                 170                 175
Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Phe
            180                 185                 190
His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
        195                 200                 205
Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
    210                 215                 220
His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
225                 230                 235
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<210> 34
<211> 2598
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24)..(1064)

<400> 34

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cctgggggggt caccctgagc cccaaagact gccaggtgtt ccgctcagac catggcagct 180
ccatctcctg tcaaccacct gccgaaatcc ccggctacct gccagccgac accgtgcacc 240
tggccgtgga attcttcaac ctgacccacc tgccagccaa cctcctccag ggcgcctcta 300
agctccaaga attgcacctc tccagcaatg ggctggaaag cctctcgccc gaattcctgc 360
ggccagtgcc gcagctgagg gtgctggatc taacccgaaa cgccctgacc gggctgccct 420
cgggcctctt ccaggcctca gccaccctgg acaccctggt attgaaagaa aaccagctgg 480
aggtcctgga ggtctcgtgg ctacacggcc tgaaagctct ggggcatctg gacctgtctg 540
ggaaccgcct ccggaaactg ccccccgggc tgctggccaa cttcaccctc ctgcgcaccc 600
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ttgaccttgg ggagaaccag ttggagacct tgccacctga cctcctgagg ggtccgctgc 660
aattagaacg gctacatcta gaaggcaaca aattgcaagt actgggaaaa gatctcctct 720
tgccgcagcc ggacctgcgc tacctcttcc tgaacggcaa caagctggcc agggtggcag 780
ccggtgcctt ccagggcctg cggcagctgg acatgctgga cctctccaat aactcactgg 840
ccagcgtgcc cgaggggctc tgggcatccc tagggcagcc aaactgggac atgcgggatg 900
gcttcgacat ctccggcaac ccctggatct gtgaccagaa cctgagcgac ctctatcgtt 960
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<212> PRT
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<400> 37

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Arg Asp Ser Ser Ser Leu Ser Ser Cys Thr Ser Gly Ile Leu Glu Glu
305 310 315 320
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<222> (41)..(586)

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<212> PRT
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Arg Gly Asp Leu Ala Asn Val Arg Val Gly Arg His Cys Val Val Lys
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Ser Arg Ser Val Ile Arg Pro Pro Phe Lys Lys Phe Ser Lys Gly Val
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Cys Val Val Asn Ala Ala Gln Ile Gly Ser Tyr Val His Val Gly Lys
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Asn Cys Val Ile Gly Arg Arg Cys Val Leu Lys Asp Cys Cys Lys Ile
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caaatctctc tcccagtaca ccagttgttc ctcccccacc tcagccctct cctgcatcct 2040
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gggacaccat acgggttggt ttcacctcct cagtcccttg cctaccccag tgagagtctg 2160
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ttcttgtttt gtctctccga aaaaaaaaaa ag 2252

<210> 41
<211> 273
<212> PRT
<213> Homo sapiens

<400> 41

Met	Ser	Gly	Ser	Gln	Ser	Glu	Val	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Arg
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			20					25					30		
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Tyr	Leu	Thr	Gln	Pro	Gly	Asn	Gly
		35					40					45			
Asn	Glu	Gly	Ser	Val	Thr	Gly	Ser	Cys	Tyr	Cys	Gly	Lys	Arg	Ile	Ser
	50					55					60				
Ser	Asp	Ser	Pro	Pro	Ser	Val	Gln	Phe	Met	Asn	Arg	Leu	Arg	Lys	His
65					70					75					80
Leu	Arg	Ala	Tyr	His	Arg	Cys	Leu	Tyr	Tyr	Thr	Arg	Phe	Gln	Leu	Leu
				85					90					95	
Ser	Trp	Ser	Val	Cys	Gly	Gly	Asn	Lys	Asp	Pro	Trp	Val	Gln	Glu	Leu
			100					105					110		
Met	Ser	Cys	Leu	Asp	Leu	Lys	Glu	Cys	Gly	His	Ala	Tyr	Ser	Gly	Ile
		115					120					125			
Val	Ala	His	Gln	Lys	His	Leu	Leu	Pro	Thr	Ser	Pro	Pro	Ile	Ser	Gln
	130					135					140				
Ala	Ser	Glu	Gly	Ala	Ser	Ser	Asp	Ile	Leu	Thr	Pro	Ala	Gln	Met	Leu
145					150					155					160
Leu	Ser	Thr	Leu	Gln	S	r	Thr	Gln	Arg	Pro	Thr	Leu	Pro	Val	Gly	Ser
					165					170					175	

Leu Ser Ser Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His
180 185 190
Thr Ala Gly His Ser Leu Ala Ala Gly Pro Glu Ala Gly Glu Asn Gln
195 200 205
Lys Gln Pro Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr
210 215 220
Val Pro Val Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala
225 230 235 240
Leu Ser Tyr Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser
245 250 255
Ser Pro Asp Leu Pro Val His Tyr Ile Pro Val Ala Pro Asp Ser Asn
260 265 270
Thr

<210> 42
<211> 3119
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (94)..(1212)

<400> 42
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ggagctctgc acgtggtgat tgtgggtggg ggctttggcg ggatcgcagc agccagccag 180
ctgcaggccc tgaacgtccc cttcatgctg gtggacatga aggactcctt ccaccacaat 240
gtggctgctc tccgagcctc cgtggagaca gggttcgcca aaaagacatt catttcttac 300
tcggtgactt tcaaggacaa cttccggcag gggctagtag tggggataga cctgaagaac 360
cagatggtgc tgctgcaggg tggcgaggcc ctgcccttct ctcatcttat cctggccacg 420
ggcagcactg ggcccttccc gggcaagttt aatgaggttt ccagccagca ggccgctatc 480
caggcctatg aggacatggt gaggcaggtc cagcgctcac ggttcatcgt ggtggtggga 540
ggaggctcgg ctggagtgga gatggcagca gagattaaaa cagaatatcc tgagaaagag 600
gtcactctca ttcactccca agtggccctg gctgacaagg agctcctgcc ctccgtccgg 660
caggaagtga aggagatcct cctccggaag ggcgtgcagc tgctgctgag tgagcgggtg 720
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aaaggcacag aggtggccac caacctggtg attctctgca ccggcatcaa gatcaacagc 840
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gagcacctcc aggtggaggg ccacagcaac gtctacgcca ttggtgactg tgccgacgtg 960
aggacgccca agatggccta tcttgccggc ctccacgcca acatcgccgt ggccaacatc 1020
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ctgtccatgg ggagaaatga cggtgtgggc caaatcagtg gcttctatgt gggccggctc 1140
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cagtctccac cttgatggag aggccaggcg ggagaactac cgcagcaggt gggcgtacgg 1260
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aagatgccaa tgatgtggtg gctagaaatg caacttgtat aaaacaaaaa tgggagagag 1380
agaggtatta aacaaatacc ccccttagag gatactttct gggtttggaa ggtgtgcttg 1440
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cagcccttcc tctgcacctg cctcctctgg gatgtgcatg tgtgtgtatg tgcttgtggt 1560
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ttatttttga gacagtctcg ccctgtcacc caggctggag tgcagtggca cgatctcagc 1920
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ttggcctctc gaagtgctgg gattccaggc gtgagccact gcggccagca catttccact 2160
tttagatcct actccatacc acaggtttca tttaagaaga aagagctaga taaatgtgct 2220
cttctggtta ccccaccctg acagagtgca tttttacacg gctagcaggg gttgagactg 2280
cagcctggcc tgccagccat tggaggtgtt taaggaaggg cagataatgt gactctttgc 2340
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cccagtgtgt gagcgacagg ccttcttcta ttgacttaca atattctaga aggacctacg 3060
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<210> 43
<211> 373
<212> PRT
<213> Homo sapiens

<400> 43

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            20                  25                  30
Leu Asn Val Pro Phe Met Leu Val Asp Met Lys Asp Ser Phe His His
        35                  40                  45
Asn Val Ala Ala Leu Arg Ala Ser Val Glu Thr Gly Phe Ala Lys Lys
    50                  55                  60
Thr Phe Ile Ser Tyr Ser Val Thr Phe Lys Asp Asn Phe Arg Gln Gly
65                  70                  75                  80
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Leu Val Val Gly Ile Asp Leu Lys Asn Gln Met Val Leu Leu Gln Gly
                 85                  90                  95
Gly Glu Ala Leu Pro Phe Ser His Leu Ile Leu Ala Thr Gly Ser Thr
            100                 105                 110
Gly Pro Phe Pro Gly Lys Phe Asn Glu Val Ser Ser Gln Gln Ala Ala
        115                 120                 125
Ile Gln Ala Tyr Glu Asp Met Val Arg Gln Val Gln Arg Ser Arg Phe
    130                 135                 140
Ile Val Val Val Gly Gly Gly Ser Ala Gly Val Glu Met Ala Ala Glu
145                 150                 155                 160
Ile Lys Thr Glu Tyr Pro Glu Lys Glu Val Thr Leu Ile His Ser Gln
                165                 170                 175
Val Ala Leu Ala Asp Lys Glu Leu Leu Pro Ser Val Arg Gln Glu Val
            180                 185                 190
Lys Glu Ile Leu Leu Arg Lys Gly Val Gln Leu Leu Leu Ser Glu Arg
        195                 200                 205
Val Ser Asn Leu Glu Glu Leu Pro Leu Asn Glu Tyr Arg Glu Tyr Ile
    210                 215                 220
Lys Val Gln Thr Asp Lys Gly Thr Glu Val Ala Thr Asn Leu Val Ile
225                 230                 235                 240
Leu Cys Thr Gly Ile Lys Ile Asn Ser Ser Ala Tyr Arg Lys Ala Phe
                245                 250                 255
Glu Ser Arg Leu Ala Ser Ser Gly Ala Leu Arg Val Asn Glu His Leu
            260                 265                 270
Gln Val Glu Gly His Ser Asn Val Tyr Ala Ile Gly Asp Cys Ala Asp
        275                 280                 285
Val Arg Thr Pro Lys Met Ala Tyr Leu Ala Gly Leu His Ala Asn Ile
    290                 295                 300
Ala Val Ala Asn Ile Val Asn Ser Val Lys Gln Arg Pro Leu Gln Ala
305                 310                 315                 320
Tyr Lys Pro Gly Ala Leu Thr Phe Leu Leu Ser Met Gly Arg Asn Asp
                325                 330                 335
Gly Val Gly Gln Ile Ser Gly Phe Tyr Val Gly Arg Leu Met Val Arg
            340                 345                 350
Leu Thr Lys Ser Arg Asp Leu Phe Val Ser Thr Ser Trp Lys Thr Met
        355                 360                 365
Arg Gln Ser Pro Pro
    370
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<210> 44
<211> 3111
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (39)..(2762)

<400> 44
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gacgtgcagc tgcgaagtgc ttggatgccg tagttagcac aaggcatgaa atgcttccag 180
aattctacaa gaccgtctct cctgcactaa tatccagatt taaagagcgt gaagagaatg 240
taaaggcaga tgtttttcac gcataccttt ctcttttgaa gcaaactcgt cctgtacaaa 300
gttggctatg tgaccctgat gcaatggagc agggagaaac acctttaaca atgcttcaga 360
gtcaggttcc caacattgtt aaagctcttc acaaacagat gaaagaaaaa agtgtgaaga 420
cccgacagtg ttgttttaac atattaactg agctggtaaa tgtattacct ggggccctaa 480
ctcaacacat tcctgtactt gtaccaggaa tcattttctc actgaatgat aaatcaagct 540
catcgaattt gaagatcgat gctttgtcat gtctatacgt aatcctctgt aaccattctc 600
ctcaagtctt ccatcctcac gttcaggctt tggttcctcc agtggtggct tgtgttggag 660
acccatttta caaaattaca tctgaggcac ttcttgttac tcaacagctt gtcaaagtaa 720
ttcgtccttt agatcagcct tcctcgtttg atgcaactcc ttatatcaaa gatctattta 780
cctgtaccat taagagatta aaagcagctg acattgatca ggaagtcaag gaaagggcta 840
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atacacttca gattttcttg gagagactaa agaatgaaat taccaggtta actacagtaa 960
aggcattgac actgattgct gggtcacctt tgaagataga tttgaggcct gttctgggag 1020
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aagaagtcaa atcagctgca tcctatgcat taggcagcat tagtgtgggc aaccttcctg 1740
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catttaaaca tacggttgat gatggtctgg atattagaaa ggcagcattt gagtgtatgt 2340
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agcaacattt gaaatggaaa ctagaagtta ggattttatg gagtatggag atagggtcca 3060
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<210> 45
<211> 908
<212> PRT
<213> Homo sapiens

<400> 45

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             20                  25                  30
Lys Cys Leu Asp Ala Val Val Ser Thr Arg His Glu Met Leu Pro Glu
         35                  40                  45
Phe Tyr Lys Thr Val Ser Pro Ala Leu Ile Ser Arg Phe Lys Glu Arg
     50                  55                  60
Glu Glu Asn Val Lys Ala Asp Val Phe His Ala Tyr Leu Ser Leu Leu
 65                  70                  75                  80
Lys Gln Thr Arg Pro Val Gln Ser Trp Leu Cys Asp Pro Asp Ala Met
                 85                  90                  95
Glu Gln Gly Glu Thr Pro Leu Thr Met Leu Gln Ser Gln Val Pro Asn
            100                 105                 110
Ile Val Lys Ala Leu His Lys Gln Met Lys Glu Lys Ser Val Lys Thr
        115                 120                 125
Arg Gln Cys Cys Phe Asn Ile Leu Thr Glu Leu Val Asn Val Leu Pro
    130                 135                 140
Gly Ala Leu Thr Gln His Ile Pro Val Leu Val Pro Gly Ile Ile Phe
145                 150                 155                 160
Ser Leu Asn Asp Lys Ser Ser Ser Ser Asn Leu Lys Ile Asp Ala Leu
                165                 170                 175
Ser Cys Leu Tyr Val Ile Leu Cys Asn His Ser Pro Gln Val Phe His
            180                 185                 190
Pro His Val Gln Ala Leu Val Pro Pro Val Val Ala Cys Val Gly Asp
        195                 200                 205
Pro Phe Tyr Lys Ile Thr Ser Glu Ala Leu Leu Val Thr Gln Gln Leu
    210                 215                 220
Val Lys Val Ile Arg Pro Leu Asp Gln Pro Ser Ser Phe Asp Ala Thr
225                 230                 235                 240
Pro Tyr Ile Lys Asp Leu Phe Thr Cys Thr Ile Lys Arg Leu Lys Ala
                245                 250                 255
Ala Asp Ile Asp Gln Glu Val Lys Glu Arg Ala Ile Ser Cys Met Gly
            260                 265                 270
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Gln Ile Ile Cys Asn Leu Gly Asp Asn Leu Gly Ser Asp Leu Pro Asn
        275                 280                 285
Thr Leu Gln Ile Phe Leu Glu Arg Leu Lys Asn Glu Ile Thr Arg Leu
    290                 295                 300
Thr Thr Val Lys Ala Leu Thr Leu Ile Ala Gly Ser Pro Leu Lys Ile
305                 310                 315                 320
Asp Leu Arg Pro Val Leu Gly Glu Gly Val Pro Ile Leu Ala Ser Phe
                325                 330                 335
Leu Arg Lys Asn Gln Arg Ala Leu Lys Leu Gly Thr Leu Ser Ala Leu
            340                 345                 350
Asp Ile Leu Ile Lys Asn Tyr Ser Asp Ser Leu Thr Ala Ala Met Ile
        355                 360                 365
Asp Ala Val Leu Asp Glu Leu Pro Pro Leu Ile Ser Glu Ser Asp Met
    370                 375                 380
His Val Ser Gln Met Ala Ile Ser Phe Leu Thr Thr Leu Ala Lys Val
385                 390                 395                 400
Tyr Pro Ser Ser Leu Ser Lys Ile Ser Gly Ser Ile Leu Asn Glu Leu
                405                 410                 415
Ile Gly Leu Val Arg Ser Pro Leu Leu Gln Gly Gly Ala Leu Ser Ala
            420                 425                 430
Met Leu Asp Phe Phe Gln Ala Leu Val Val Thr Gly Thr Asn Asn Leu
        435                 440                 445
Gly Tyr Met Asp Leu Leu Arg Met Leu Thr Gly Pro Val Tyr Ser Gln
    450                 455                 460
Ser Thr Ala Leu Thr His Lys Gln Ser Tyr Tyr Ser Ile Ala Lys Cys
465                 470                 475                 480
Val Ala Ala Leu Thr Arg Ala Cys Pro Lys Glu Gly Pro Ala Val Val
                485                 490                 495
Gly Gln Phe Ile Gln Asp Val Lys Asn Ser Arg Ser Thr Asp Ser Ile
            500                 505                 510
Arg Leu Leu Ala Leu Leu Ser Leu Gly Glu Val Gly His His Ile Asp
        515                 520                 525
Leu Ser Gly Gln Leu Glu Leu Lys Ser Val Ile Leu Glu Ala Phe Ser
    530                 535                 540
Ser Pro Ser Glu Glu Val Lys Ser Ala Ala Ser Tyr Ala Leu Gly Ser
545                 550                 555                 560
Ile Ser Val Gly Asn Leu Pro Glu Tyr Leu Pro Phe Val Leu Gln Glu
                565                 570                 575
Ile Thr Ser Gln Pro Lys Arg Gln Tyr Leu Leu Leu His Ser Leu Lys
            580                 585                 590
Glu Ile Ile Ser Ser Ala Ser Val Val Gly Leu Lys Pro Tyr Val Glu
        595                 600                 605
Asn Ile Trp Ala Leu Leu Leu Lys His Cys Glu Cys Ala Glu Glu Gly
    610                 615                 620
Thr Arg Asn Val Val Ala Glu Cys Leu Gly Lys Leu Thr Leu Ile Asp
625                 630                 635                 640
Pro Glu Thr Leu Leu Pro Arg Leu Lys Gly Tyr Leu Ile Ser Gly Ser
                645                 650                 655
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Ser Tyr Ala Arg Ser Ser Val Val Thr Ala Val Lys Phe Thr Ile Ser
660 665 670
Asp His Pro Gln Pro Ile Asp Pro Leu Leu Lys Asn Cys Ile Gly Asp
675 680 685
Phe Leu Lys Thr Leu Glu Asp Pro Asp Leu Asn Val Arg Arg Val Ala
690 695 700
Leu Val Thr Phe Asn Ser Ala Ala His Asn Lys Pro Ser Leu Ile Arg
705 710 715 720
Asp Leu Leu Asp Thr Val Leu Pro His Leu Tyr Asn Glu Thr Lys Val
725 730 735
Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys His Thr
740 745 750
Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys Met Tyr
755 760 765
Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu Phe Leu
770 775 780
Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys Met Leu
785 790 795 800
Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser Ala Val
805 810 815
Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr Cys Thr
820 825 830
Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys Gln Asp
835 840 845
Glu Leu Lys Arg Ser Ala Thr Arg Ala Val Ala Ala Leu Leu Thr Ile
850 855 860
Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser Gln Ile
865 870 875 880
Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln Lys Asp
885 890 895
Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser
900 905

<210> 46
<211> 1599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (156)..(623)

<400> 46
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cgccgccgcc cttcgagggc gccccaggcc gcgccatggt gaaggtgacg ttcaactccg 180
ctctggccca gaaggaggcc aagaaggacg agcccaagag cggcgaggag gcgctcatca 240

tccccccga cgccgtcgcg gtggactgca aggacccaga tgatgtggta ccagttggcc 300
aaagaagagc ctggtgttgg tgcatgtgct ttggactagc atttatgctt gcaggtgtta 360
ttctaggagg agcatacttg tacaaatatt ttgcacttca accagatgac gtgtactact 420
gtggaataaa gtacatcaaa gatgatgtca tcttaaatga gccctctgca gatgccccag 480
ctgctctcta ccagacaatt gaagaaaata ttaaaatctt tgagaagaag aagttgaatt 540
tatcagtgtg cctgtcccag agtttgcaga tagtgatcct gccaacattg ttcatgactt 600
taacaagaaa cttacagcct atttagatct taacctggat aagtgctatg tgatccctct 660
gaacacttcc attgttatgc cacccagaaa cctactggag ttacttatta acatcaaggc 720
tggaacctat ttgcctcagt cctatctgat tcatgagcac atggttatta ctgatcgcat 780
tgaaaacatt gatcacctgg gtttctttat ttatcgactg tgtcatgaca aggaaactta 840
caaactgcaa cgcagagaaa ctattaaagg tattcagaaa cgtgaagcca gcaattgttt 900
cgcaattcgg cattttgaaa acaaatttgc cgtggaaact ttaatttgtt cttgaacagt 960
caagaaaaac attattgagg aaaattaata tcacagcata accccaccct ttacattttg 1020
tgcagtgatt atttttaaa gtcttctttc atgtaagtag caaacagggc tttactatct 1080
tttcatctca ttaattcaat taaaaccatt accttaaaat ttttttcttt cgaagtgtgg 1140
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<210> 47
<211> 156
<212> PRT
<213> Homo sapiens

<400> 47
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20 25 30
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35 40 45
Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50 55 60
Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65 70 75 80
Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
85 90 95
Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100 105 110
Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Lys Lys Lys Leu Asn
115 120 125
Leu Ser Val Cys Leu Ser Gln Ser Leu Gln Ile Val Ile Leu Pro Thr

130 135 140
Leu Phe Met Thr Leu Thr Arg Asn Leu Gln Pro Ile
145 150 155

<210> 48
<211> 3733
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (20)..(1000)

<400> 48
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tttaaaaaat gct 3733

<210> 49
<211> 327
<212> PRT
<213> Homo sapiens

<400> 49
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20 25 30
Phe Ser Ser Leu Ser Pro Met Ala Arg Lys Ile Met Gln Asp Lys Glu
35 40 45
Lys Ile Arg Glu Lys Tyr Gly Pro Glu Trp Ala Arg Leu Pro Pro Ala
50 55 60
Gln Gln Asp Glu Ile Ile Asp Arg Cys Leu Val Gly Pro Arg Ala Pro
65 70 75 80

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Ala Pro Arg Asp Pro Gly Asp Ser Glu Glu Leu Thr Arg Ph  Pro Gly
                 85                  90                  95
Leu Arg Gly Pro Thr Gly Gln Lys Val Val Arg Phe Gly Asp Glu Asp
            100                 105                 110
Leu Thr Trp Gln Asp Glu His Ser Ala Pro Phe Ser Trp Glu Thr Lys
        115                 120                 125
Ser Gln Met Glu Phe Ser Ile Ser Ala Leu Ser Ile Gln Glu Pro Ser
    130                 135                 140
Asn Gly Thr Ala Ala Ser Glu Pro Arg Pro Leu Ser Lys Ala Ser Gln
145                 150                 155                 160
Gly Ser Gln Ala Leu Lys Ser Ser Gln Gly Ser Arg Ser Ser Ser Leu
                165                 170                 175
Asp Ala Leu Gly Pro Thr Arg Lys Glu Glu Glu Ala Ser Phe Trp Lys
            180                 185                 190
Ile Asn Ala Glu Arg Ser Arg Gly Glu Gly Pro Glu Ala Glu Phe Gln
        195                 200                 205
Ser Leu Thr Pro Ser Gln Ile Lys Ser Met Glu Lys Gly Glu Lys Val
    210                 215                 220
Leu Pro Pro Cys Tyr Arg Gln Glu Pro Ala Pro Lys Asp Arg Glu Ala
225                 230                 235                 240
Lys Val Glu Arg Pro Ser Thr Leu Arg Gln Glu Gln Arg Pro Leu Pro
                245                 250                 255
Asn Val Ser Thr Glu Arg Glu Arg Pro Gln Pro Val Gln Ala Phe Ser
            260                 265                 270
Ser Ala Leu His Glu Ala Ala Pro Ser Gln Leu Glu Gly Lys Leu Pro
        275                 280                 285
Ser Pro Asp Val Arg Gln Asp Asp Gly Glu Asp Thr Leu Phe Ser Glu
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Pro Lys Phe Ala Gln Val Ser Ser Ser Asn Val Val Leu Lys Thr Gly
305                 310                 315                 320
Phe Asp Phe Leu Asp Asn Trp
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<210> 50
<211> 1881
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (141)..(1214)

<400> 50
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tgtaaactct gatttgcagg atggctggct gtggtgaaat tgatcattca ataaacatgc 180
ttcctacaaa caggaaagcg aacgagtcct gttctaatac tgcaccttct ttaaccgtcc 240

ctgaatgtgc catttgtctg caaacatgtg ttcatccagt cagtctgccc tgtaagcacg 300
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gacaagaaat tcccgaggat ttccttgaca agccaacctt gttgtcacca gaagaactca 420
aggcagcaag tagaggaaat ggtgaatatg catggtatta tgaaggaaga aatgggtggt 480
ggcagtacga tgagcgcact agtagagagc tggaagatgc tttttccaaa ggtaaaaaga 540
acactgaaat gttaattgct ggctttctgt atgtcgctga tcttgaaaac atggttcaat 600
ataggagaaa tgaacatgga cgtcgcagga agattaagcg agatataata gatataccaa 660
agaagggagt agctggactt aggctagact gtgatgctaa taccgtaaac ctagcaagag 720
agagctctgc tgacggagcg gacagtgtat cagcacagag tggagcttct gttcagcccc 780
tagtgtcttc tgtaaggccc ctaacatcag tagatggtca gtcaacaagc cctgcaacac 840
catcccctga tgcaagcact tctctggaag actcttttgc tcatttacaa ctcagtggag 900
acaacacagc tgaaaggagt cataggggag aaggagaaga agatcatgaa tcaccatctt 960
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cagtaactga agtttaaata aaaatgtctt cagctccatg ctcaaggttg aaagggttac 1260
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taataaatac tagagtttat c 1881

<210> 51
<211> 358
<212> PRT
<213> Homo sapiens

<400> 51

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			20					25					30		
Val	Pro	Glu	Cys	Ala	Ile	Cys	Leu	Gln	Thr	Cys	Val	His	Pro	Val	Ser
		35					40					45			
Leu	Pro	Cys	Lys	His	Val	Phe	Cys	Tyr	Leu	Cys	Val	Lys	Gly	Ala	Ser
	50					55					60				
Trp	Leu	Gly	Lys	Arg	Cys	Ala	Leu	Arg	Arg	Gln	Glu	Ile	Pro	Glu	Asp
65					70					75					80
Phe	Leu	Asp	Lys	Pro	Thr	Leu	Leu	Ser	Pro	Glu	Glu	Leu	Lys	Ala	Ala
				85					90					95	

Ser Arg Gly Asn Gly Glu Tyr Ala Trp Tyr Tyr Glu Gly Arg Asn Gly
100 105 110
Trp Trp Gln Tyr Asp Glu Arg Thr Ser Arg Glu Leu Glu Asp Ala Phe
115 120 125
Ser Lys Gly Lys Lys Asn Thr Glu Met Leu Ile Ala Gly Phe Leu Tyr
130 135 140
Val Ala Asp Leu Glu Asn Met Val Gln Tyr Arg Arg Asn Glu His Gly
145 150 155 160
Arg Arg Arg Lys Ile Lys Arg Asp Ile Ile Asp Ile Pro Lys Lys Gly
165 170 175
Val Ala Gly Leu Arg Leu Asp Cys Asp Ala Asn Thr Val Asn Leu Ala
180 185 190
Arg Glu Ser Ser Ala Asp Gly Ala Asp Ser Val Ser Ala Gln Ser Gly
195 200 205
Ala Ser Val Gln Pro Leu Val Ser Ser Val Arg Pro Leu Thr Ser Val
210 215 220
Asp Gly Gln Ser Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser Thr
225 230 235 240
Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn Thr
245 250 255
Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser Pro
260 265 270
Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr Glu
275 280 285
Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala Gln
290 295 300
His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln Thr
305 310 315 320
Val Pro Asp Arg Ser Asp Arg Leu Gly Thr Asp Arg Ser Val Ala Gly
325 330 335
Gly Gly Thr Val Ser Val Ser Val Arg Ser Arg Arg Pro Asp Gly Gln
340 345 350
Cys Thr Val Thr Glu Val
355

<210> 52
<211> 1824
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (208)..(1824)

<400> 52
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tacaagacca cggatgacat cgtgaaggtt gaagtctggg atgtagtaga caaaggaaaa 180
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ggcaaaaccc cctctaagga gaag 1824

<210> 53
<211> 539
<212> PRT
<213> Homo sapiens

<400> 53
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Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val Met Met Phe
20 25 30
Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg Glu Leu Pro
35 40 45
Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn Tyr Arg Asp
50 55 60
Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg Asp Phe Ile
65 70 75 80
Asp Asn Leu Asp Arg Pr Pro Gly Ser Ser Tyr Phe Arg Tyr Ala Glu

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                  85                  90                  95
Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His Lys Phe Phe
             100                 105                 110
Asn Ile Pro Ser Leu Gln Leu Gln Arg Glu Thr Leu Leu Arg Gln Leu
         115                 120                 125
Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu Leu Ser Val
     130                 135                 140
Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu Glu Met Met
145                 150                 155                 160
Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala Asn Gly Gln
                165                 170                 175
Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Val Pro Ala Gly Ala Val
             180                 185                 190
Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala Pro Gln Leu
         195                 200                 205
Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val Pro Pro Ser
     210                 215                 220
Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala Pro Arg Arg
225                 230                 235                 240
Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr Glu Ala Ala
                245                 250                 255
Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro Ala Thr Val
             260                 265                 270
Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp Arg Ser Phe
         275                 280                 285
Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val Gly Ala Lys
     290                 295                 300
Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu Gly Gly Asn
305                 310                 315                 320
Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu Asp Gln Pro
                325                 330                 335
Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser Gln Asp Ile
             340                 345                 350
Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro Thr Lys Gly
         355                 360                 365
Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr Lys Trp Ser
     370                 375                 380
Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro Thr Arg Thr
385                 390                 395                 400
Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr Gly Pro Glu
                405                 410                 415
Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro Gly Lys Gly
             420                 425                 430
Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro Ile Ala Ala
         435                 440                 445
Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu Ser Glu Gly
     450                 455                 460
Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg Asp Asp Pro
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465                 470                 475                 480
Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro Pro Pro Pro
                485                 490                 495
Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp Ser Asp Leu
            500                 505                 510
Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser Ser Glu Glu
        515                 520                 525
Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys
    530                 535
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<210> 54
<211> 1518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (8)..(1432)

<400> 54
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aatccagttt gaaagaaatt ttgatcggca gaaaagtcgc atcctgagtc tcagctggca 180
tccctctggt acccacattg cagctggttc catagactac attagtgtgt ttgatgtcaa 240
atcaggcagc gctgttcata agatgattgt ggacaggcag tatatgggcg tgtctaagcg 300
gaagtgcatc gtgtggggtg tcgccttctt gtccgatggc actatcataa gtgtggactc 360
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cacagccgag ggaacagtct tccattttca gctggtccct gtgacatcta acagcagtga 540
gaagcagtgg gtgcggacaa aaccgttcca gcatcacact catgacgtgc gcactgtggc 600
ccacagccca acagcgctga tatctggagg cactgacacc cacttagtct ttcgtcctct 660
catggagaag gtggaagtaa agaattacga tgccgctctc cgaaaaatca cctttcccca 720
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<212> PRT
<213> Homo sapiens

<400> 55

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Gln Ile Thr Pro Asp Lys Ile Gln Phe Glu Arg Asn Phe Asp Arg Gln
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Lys Ser Arg Ile Leu Ser Leu Ser Trp His Pro Ser Gly Thr His Ile
    50                  55                  60
Ala Ala Gly Ser Ile Asp Tyr Ile Ser Val Phe Asp Val Lys Ser Gly
65                  70                  75                  80
Ser Ala Val His Lys Met Ile Val Asp Arg Gln Tyr Met Gly Val Ser
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Lys Arg Lys Cys Ile Val Trp Gly Val Ala Phe Leu Ser Asp Gly Thr
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Ile Ile Ser Val Asp Ser Ala Gly Lys Val Gln Phe Trp Asp Ser Ala
        115                 120                 125
Thr Gly Thr Leu Val Lys Ser His Leu Ile Ala Asn Ala Asp Val Gln
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145                 150                 155                 160
Glu Gly Thr Val Phe His Phe Gln Leu Val Pro Val Thr Ser Asn Ser
                165                 170                 175
Ser Glu Lys Gln Trp Val Arg Thr Lys Pro Phe Gln His His Thr His
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Asp Val Arg Thr Val Ala His Ser Pro Thr Ala Leu Ile Ser Gly Gly
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Thr Asp Thr His Leu Val Phe Arg Pro Leu Met Glu Lys Val Glu Val
    210                 215                 220
Lys Asn Tyr Asp Ala Ala Leu Arg Lys Ile Thr Phe Pro His Arg Cys
225                 230                 235                 240
Leu Ile Ser Cys Ser Lys Lys Arg Gln Leu Leu Leu Phe Gln Phe Ala
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His His Leu Glu Leu Trp Arg Leu Gly Ser Thr Val Ala Thr Gly Thr
            260                 265                 270
Val Glu Ala Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu
        275                 280                 285
Ala Ala Ser Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln
    290                 295                 300
Leu Lys Leu His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala
305                 310                 315                 320
Met Ala Ile Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp
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Gln Gln Val Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp
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Ser Arg Thr Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg
        355                 360                 365
Asp Thr Pro Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His
    370                 375                 380
Ile Leu Leu His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu
385                 390                 395                 400
Pro Leu Pro Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr
                405                 410                 415
Asn Glu Ser Asp Val Ile Arg Arg Arg Thr Ala His Ala Phe Lys Ile
            420                 425                 430
Ser Lys Ile Tyr Lys Pro Leu Leu Phe Met Asp Leu Leu Asp Glu Arg
        435                 440                 445
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (26)..(709)

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cggcttcagc ctgggcgtgt tcctgctcaa gagcggcacg tccatcccgc tgcacgacca 240
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gcgcccagga gcggtgggcc gaagacgtgc cctaccctac cacaagggct gtgtctctac 780
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gcaggggact atctgaagcg cttccatcct aaagccataa tgaaaatatc ttcctctctt 1020
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<210> 57
<211> 228
<212> PRT
<213> Homo sapiens

<400> 57

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			20					25					30		
Leu	Gln	Pro	Leu	Pro	Pro	Asn	Leu	Pro	Pro	Val	Thr	Tyr	Met	His	Ile
		35					40					45			
Tyr	Glu	Thr	Asp	Gly	Phe	Ser	Leu	Gly	Val	Phe	Leu	Leu	Lys	Ser	Gly
	50					55					60				
Thr	Ser	Ile	Pro	Leu	His	Asp	His	Pro	Gly	Met	His	Gly	Met	Leu	Lys
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Val	Leu	Tyr	Gly	Thr	Val	Arg	Ile	Ser	Cys	Met	Asp	Lys	Leu	Asp	Ala
				85					90					95	
Gly	Gly	Gly	Gln	Arg	Pro	Arg	Ala	Leu	Pro	Pro	Glu	Gln	Gln	Phe	Glu
			100					105					110		
Pro	Pro	Leu	Gln	Pro	Arg	Glu	Arg	Glu	Ala	Val	Arg	Pro	Gly	Val	Leu
		115					120					125			
Arg	Ser	Arg	Ala	Glu	Tyr	Thr	Glu	Ala	Ser	Gly	Pro	Cys	Ile	Leu	Thr
	130					135					140				
Pro	His	Arg	Asp	Asn	Leu	His	Gln	Ile	Asp	Ala	Val	Glu	Gly	Pro	Ala
145					150					155					160

Ala Phe Leu Asp Ile Leu Ala Pro Pro Tyr Asp Pro Asp Asp Gly Arg
165 170 175
Asp Cys His Tyr Tyr Arg Val Leu Glu Pro Val Arg Pro Lys Glu Ala
180 185 190
Ser Ser Ser Ala Cys Asp Leu Pro Arg Glu Val Trp Leu Leu Glu Thr
195 200 205
Pro Gln Ala Asp Asp Phe Trp Cys Glu Gly Glu Pro Tyr Pro Gly Pro
210 215 220
Lys Val Phe Pro
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<210> 58
<211> 2661
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (6)..(2045)

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ccccagtacc accgccaggt ccattgccac ccagtctccc acctgttaca ggaccaccac 240
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ctgttcctac tgtagtaaca actggcattc atcaccagcc tcctcctgct ccaccctctc 360
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<210> 59
<211> 680
<212> PRT
<213> Homo sapiens

<400> 59
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35 40 45
Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro Pro
50 55 60
Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro Pro
65 70 75 80
Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser Ala
85 90 95
Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln Pro
100 105 110
Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr Asp
115 120 125
Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro Met
130 135 140
Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu Thr
145 150 155 160
Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys Ser

165 170 175
Ser Met Arg Ile Val Val Asp Ser Glu Ser Arg Lys Arg Thr Ile Gly
180 185 190
Ser Gly Glu Pro Gly Val Pro Thr Lys Lys Thr Trp Phe Asp Lys Pro
195 200 205
Asn Phe Asn Arg Thr Asn Ser Pro Gly Phe Gln Lys Lys Val Gln Phe
210 215 220
Gly Asn Glu Asn Thr Lys Leu Glu Leu Arg Lys Val Pro Pro Glu Leu
225 230 235 240
Asn Asn Ile Ser Lys Leu Asn Glu His Phe Ser Arg Phe Gly Thr Leu
245 250 255
Val Asn Leu Gln Val Ala Tyr Asn Gly Asp Pro Glu Gly Ala Leu Ile
260 265 270
Gln Phe Ala Thr Tyr Glu Glu Ala Lys Lys Ala Ile Ser Ser Thr Glu
275 280 285
Ala Val Leu Asn Asn Arg Phe Ile Lys Val Tyr Trp His Arg Glu Gly
290 295 300
Ser Thr Gln Gln Leu Gln Thr Thr Ser Pro Lys Val Met Gln Pro Leu
305 310 315 320
Val Gln Gln Pro Ile Leu Pro Val Val Lys Gln Ser Val Lys Glu Arg
325 330 335
Leu Gly Pro Val Pro Ser Ser Thr Ile Glu Pro Ala Glu Ala Gln Ser
340 345 350
Ala Ser Ser Asp Leu Pro Gln Val Leu Ser Thr Ser Thr Gly Leu Thr
355 360 365
Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr Leu
370 375 380
Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys Lys
385 390 395 400
Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln Glu
405 410 415
Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys Leu
420 425 430
Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys
435 440 445
Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val
450 455 460
Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys
465 470 475 480
Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys
485 490 495
Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr
500 505 510
Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg
515 520 525
Gly Arg Gly Il His Ser Arg Gly Arg Gly Ala Val His Gly Arg Gly
530 535 540
Arg Gly Arg Gly Arg Gly Arg Gly Val Pro Gly His Ala Val Val Asp

545 550 555 560
His Arg Pro Arg Ala Leu Glu Ile Ser Ala Phe Thr Glu Ser Asp Arg
565 570 575
Glu Asp Leu Leu Pro His Phe Ala Gln Tyr Gly Glu Ile Glu Asp Cys
580 585 590
Gln Ile Asp Asp Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr Arg
595 600 605
Ala Glu Ala Glu Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln
610 615 620
Asp Leu Lys Leu Ala Trp Asn Lys Pro Val Thr Asn Ile Ser Ala Val
625 630 635 640
Glu Thr Glu Glu Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu Ser
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<210> 60
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<212> DNA
<213> Homo sapiens

<220>
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<222> (137)..(844)

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<210> 61
<211> 236
<212> PRT
<213> Homo sapiens

<400> 61

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			20					25					30		
Ser	Gly	Ser	Asn	Ser	Leu	Leu	Ser	Lys	Leu	Ile	His	Gln	Ser	Tyr	His
		35					40					45			
Gly	Thr	Met	Asp	Thr	Val	Ser	Leu	Ser	Gly	Thr	Ile	Pro	Val	Gln	Met
	50					55					60				
Leu	Leu	Glu	Ile	Gly	Leu	Asp	Lys	Leu	Lys	Lys	Asp	Tyr	Ile	Ser	Phe
65					70					75					80
Phe	Ile	Gly	Gln	Glu	Leu	Ala	Ser	Leu	Asn	His	Leu	Glu	Tyr	Phe	Ile
				85					90					95	
Ala	Pro	Ser	Val	Asp	Ile	Gln	Glu	Gln	Val	Tyr	Arg	Val	Gln	Lys	Leu
			100					105					110		
His	His	Ile	Leu	Glu	Ile	Leu	Val	Ser	Cys	Met	Pro	Phe	Ile	Lys	Ser
		115					120					125			
Gln	His	Glu	Leu	Leu	Phe	Ser	Leu	Thr	Gln	Ile	Cys	Ile	Lys	Tyr	Tyr
	130					135					140				
Lys	Gln	Asn	Pro	Leu	Asp	Glu	Gln	His	Ile	Phe	Gln	Leu	Pro	Val	Arg
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Pro	Thr	Ala	Val	Lys	Asn	Leu	Tyr	Gln	Ser	Glu	Lys	Pro	Gln	Lys	Trp
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Arg	Val	Glu	Ile	Tyr	Ser	Gly	Gln	Lys	Lys	Ile	Lys	Thr	Val	Trp	Gln
			180					185					190		
Leu	Ser	Asp	Ser	Ser	Pro	Ile	Asp	His	Leu	Asn	Phe	His	Lys	Pro	Asp

195 200 205
Phe Ser Glu Leu Thr Leu Asn Gly Ser Leu Glu Glu Arg Ile Phe Phe
210 215 220
Thr Asn Met Val Thr Cys Ser Gln Val His Phe Lys
225 230 235

<210> 62
<211> 2279
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (97)..(1650)

<400> 62
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gtatcccttt ccatgacccg acctgtgtct attgaggggt ccgaggaata ccagcgtaag 180
cacctagcag cccatggttt aacgatgctg tttgagcaca tggccacaaa ttacaagctt 240
gaatttacag cacttgtggt tttttcatca ctttgggagt tgatggtccc cttcacgaga 300
gattataata ccctacagga agcactaagt aatatggatg attatgacaa aacctgcttg 360
gagtctgcat tagttggtgt ttgcaatatc gttcagcaag aatggggtgg tgcaattcct 420
tgccaggttg tcctggtgac agacggctgt cttggcattg gtagagggtc actgcgacat 480
tccctagcca ctcaaaatca acgaagtgag agcaacaggt ttccactacc ttttcctttc 540
ccatctaagt tatatatcat gtgcatggcg aatttggagg agctccagag caccgattcc 600
ttggaatgcc ttgaacgtct catatattta aacaatggtg aagggcagat ttttactatt 660
gatggccccc tgtgcttgaa gaatgtacag tctatgtttg gaaaactgat agatttggca 720
tatacgcctt tccatgctgt tctcaagtgt ggccacctaa ctgctgatgt acaagtcttc 780
cccaggccag aacctttttgt tgtagatgaa gaaattgatc ctatccctaa agtcattaac 840
acagatttgg aaatagtggg atttattgat atagctgata tttcaagtcc cccagttctg 900
tccagacatc tggtcttacc tatagcactt aacaaagaag gtgatgaggt gggtactggc 960
atcactgatg acaatgaaga tgaaaattca gccaatcaga ttgcaggcaa aatacccaac 1020
ttttgtgtcc tgctccatgg tagcctaaaa gtggaaggaa tggtagcgat tgttcaatta 1080
ggtcctgaat ggcatggaat gctctactcc caagctgaca gcaagaagaa atcaaacctc 1140
atgatgtctc tctttgagcc tggcccagaa cctctcccat ggctagggaa aatggcacag 1200
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ctactagtat gagaaggatg tgaaggtggt tggctggttg ggctttaact tcctgggatt 1860

cataattttt aagcttggaa gatagctgct gttcccatga tgggcacatt tcctgagaag 1920
cttgaatgac tgatgagcat agagcacccc tgccttcctc aggaaacctg accggcaggg 1980
gctctctggc ttcctgaaag cttcacctct tccctcgttt atatctcaac tgtaagggca 2040
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acacaccacc actaagtttc agaactttcc ttagaacttg ggcaaaatgt ggtggtaact 2160
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<210> 63
<211> 518
<212> PRT
<213> Homo sapiens

<400> 63

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 1               5                  10                  15
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            20                  25                  30
His Gly Leu Thr Met Leu Phe Glu His Met Ala Thr Asn Tyr Lys Leu
        35                  40                  45
Glu Phe Thr Ala Leu Val Val Phe Ser Ser Leu Trp Glu Leu Met Val
    50                  55                  60
Pro Phe Thr Arg Asp Tyr Asn Thr Leu Gln Glu Ala Leu Ser Asn Met
65                  70                  75                  80
Asp Asp Tyr Asp Lys Thr Cys Leu Glu Ser Ala Leu Val Gly Val Cys
                85                  90                  95
Asn Ile Val Gln Gln Glu Trp Gly Gly Ala Ile Pro Cys Gln Val Val
            100                 105                 110
Leu Val Thr Asp Gly Cys Leu Gly Ile Gly Arg Gly Ser Leu Arg His
        115                 120                 125
Ser Leu Ala Thr Gln Asn Gln Arg Ser Glu Ser Asn Arg Phe Pro Leu
    130                 135                 140
Pro Phe Pro Phe Pro Ser Lys Leu Tyr Ile Met Cys Met Ala Asn Leu
145                 150                 155                 160
Glu Glu Leu Gln Ser Thr Asp Ser Leu Glu Cys Leu Glu Arg Leu Ile
                165                 170                 175
Tyr Leu Asn Asn Gly Glu Gly Gln Ile Phe Thr Ile Asp Gly Pro Leu
            180                 185                 190
Cys Leu Lys Asn Val Gln Ser Met Phe Gly Lys Leu Ile Asp Leu Ala
        195                 200                 205
Tyr Thr Pro Phe His Ala Val Leu Lys Cys Gly His Leu Thr Ala Asp
    210                 215                 220
Val Gln Val Phe Pro Arg Pro Glu Pro Phe Val Val Asp Glu Glu Ile
225                 230                 235                 240
Asp Pro Ile Pro Lys Val Ile Asn Thr Asp Leu Glu Ile Val Gly Phe
                245                 250                 255
Ile Asp Ile Ala Asp Ile Ser Ser Pro Pro Val Leu Ser Arg His Leu
```

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            260                 265                 270
Val Leu Pro Ile Ala Leu Asn Lys Glu Gly Asp Glu Val Gly Thr Gly
        275                 280                 285
Ile Thr Asp Asp Asn Glu Asp Glu Asn Ser Ala Asn Gln Ile Ala Gly
    290                 295                 300
Lys Ile Pro Asn Phe Cys Val Leu Leu His Gly Ser Leu Lys Val Glu
305                 310                 315                 320
Gly Met Val Ala Ile Val Gln Leu Gly Pro Glu Trp His Gly Met Leu
                325                 330                 335
Tyr Ser Gln Ala Asp Ser Lys Lys Lys Ser Asn Leu Met Met Ser Leu
            340                 345                 350
Phe Glu Pro Gly Pro Glu Pro Leu Pro Trp Leu Gly Lys Met Ala Gln
        355                 360                 365
Leu Gly Pro Ile Ser Asp Ala Lys Glu Asn Pro Tyr Gly Glu Asp Asp
    370                 375                 380
Asn Lys Ser Pro Phe Pro Leu Gln Pro Lys Asn Lys Arg Ser Tyr Ala
385                 390                 395                 400
Gln Asn Val Thr Val Trp Ile Lys Pro Ser Gly Leu Gln Thr Asp Val
                405                 410                 415
Gln Lys Ile Leu Arg Asn Ala Arg Lys Leu Pro Glu Lys Thr Gln Thr
            420                 425                 430
Phe Tyr Lys Glu Leu Asn Arg Leu Arg Lys Ala Ala Leu Ala Phe Gly
        435                 440                 445
Phe Leu Asp Leu Leu Lys Gly Val Ala Asp Met Leu Glu Arg Glu Cys
    450                 455                 460
Thr Leu Leu Pro Glu Thr Ala His Pro Asp Ala Ala Phe Gln Leu Thr
465                 470                 475                 480
His Ala Ala Gln Gln Leu Lys Leu Ala Ser Thr Gly Thr Ser Glu Tyr
                485                 490                 495
Ala Ala Tyr Asp Gln Asn Ile Thr Pro Leu His Thr Asp Phe Ser Gly
            500                 505                 510
Ser Ser Thr Glu Arg Ile
        515
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<210> 64
<211> 2155
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (65)..(1405)

<400> 64
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cccgcacgca atctgcctcg gagacgttga taacgatacg ttaaatgaac tggtggtggg 180

agacaccagc gggaaggtgt ctgtgtataa aaatgatgac agtcggccat ggctcacctg 240
ttcctgccag ggaatgctga cttgcgctgg ggttggagac gtgtgtaata aaggaaagaa 300
cctgttggtg gcagtgagtg ctgaaggctg gtttcatttg tttgacctga cacctgccaa 360
ggtgttggat gcttctgggc accacgagac actaatcgga gaggagcagc gtccagtctt 420
caagcagcac atccctgcca acaccaaggt catgctgatc agcgacatcg atggagatgg 480
gtgtcgtgag ctggtggtgg gctacacaga ccgtgtggtg cgagctttcc gctgggagga 540
gctaggtgag ggtcctgaac atctgacagg gcagctggtg tccctcaaga aatggatgct 600
ggagggtcag gtggacagcc tctcagtgac tctggggcca ctgggtcttc ctgaactgat 660
ggtgtctcag ccaggttgtg cgtatgcaat tctactgtgt acctggaaaa aggacactgg 720
gtcccctcct gcctctgaag ggcccacgga tggtagtagg gagaccccag ctgcccgaga 780
cgtggtgctg caccagacat ctggccgtat ccacaacaag aatgtctcca ctcacctaat 840
tggcaacatc aaacaaggcc acggcactga gagtagtggc tctggcctct ttgccctgtg 900
caccctggat gggacactga agctcatgga agaaatggaa gaagcagaca agctgctgtg 960
gtcagtgcag gtggatcacc agctctttgc cctggagaaa ctggatgtca ccggcaacgg 1020
gcatgaggag gtagttgcat gcgcctggga tggacagaca tatatcattg atcacaaccg 1080
caccgtcgtc cgcttccaag tggatgaaaa tatccgtgcc ttctgtgcgg gcctgtacgc 1140
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tgtgtactgg gaggtgcagc tggagcggat ggagtctacc aatctggtga aactgctgga 1260
gaccaagccg gagtaccaca gcctgctgca ggagctgggc gtggatcctg acgacctccc 1320
tgtgactcgt gccctgcttc accaaacgct ctaccatcca gaccagccac cacagtgtgc 1380
tccctcaagc ctccaggatc ccacctagct gtacttgcct catagctggt gaaggattct 1440
tctgaacccc caccctaccc cctaaaggta tctgtggtat tggcaggata gggaatatgc 1500
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attgttaaag gaatggcaaa ctgttttgtt ttgaaggatc tttctacagt ctggtcttac 1920
ccatgttcct agcaaccctg agatgatttt cttccattta ccaaagcagc cgggtcagtg 1980
ccttctcacg ttgccgtatt cttcaggtat tagtcagctt cagaagccct gctcccattt 2040
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atgtgatgcg ggtttatgat ccagaccaca atcagaatta tatcttgggt cattt 2155

<210> 65
<211> 447
<212> PRT
<213> Homo sapiens

<400> 65
Met Arg Ser Val Ser Tyr Val Gln Arg Val Ala Leu Glu Phe Ser Gly
1 5 10 15
Ser Leu Phe Pro His Ala Ile Cys Leu Gly Asp Val Asp Asn Asp Thr
20 25 30
Leu Asn Glu Leu Val Val Gly Asp Thr Ser Gly Lys Val Ser Val Tyr
35 40 45
Lys Asn Asp Asp Ser Arg Pro Trp Leu Thr Cys Ser Cys Gln Gly Met

```
    50                  55                  60
Leu Thr Cys Ala Gly Val Gly Asp Val Cys Asn Lys Gly Lys Asn Leu
 65                  70                  75                  80
Leu Val Ala Val Ser Ala Glu Gly Trp Phe His Leu Phe Asp Leu Thr
                85                  90                  95
Pro Ala Lys Val Leu Asp Ala Ser Gly His His Glu Thr Leu Ile Gly
            100                 105                 110
Glu Glu Gln Arg Pro Val Phe Lys Gln His Ile Pro Ala Asn Thr Lys
        115                 120                 125
Val Met Leu Ile Ser Asp Ile Asp Gly Asp Gly Cys Arg Glu Leu Val
    130                 135                 140
Val Gly Tyr Thr Asp Arg Val Val Arg Ala Phe Arg Trp Glu Glu Leu
145                 150                 155                 160
Gly Glu Gly Pro Glu His Leu Thr Gly Gln Leu Val Ser Leu Lys Lys
                165                 170                 175
Trp Met Leu Glu Gly Gln Val Asp Ser Leu Ser Val Thr Leu Gly Pro
            180                 185                 190
Leu Gly Leu Pro Glu Leu Met Val Ser Gln Pro Gly Cys Ala Tyr Ala
        195                 200                 205
Ile Leu Leu Cys Thr Trp Lys Lys Asp Thr Gly Ser Pro Pro Ala Ser
    210                 215                 220
Glu Gly Pro Thr Asp Gly Ser Arg Glu Thr Pro Ala Ala Arg Asp Val
225                 230                 235                 240
Val Leu His Gln Thr Ser Gly Arg Ile His Asn Lys Asn Val Ser Thr
                245                 250                 255
His Leu Ile Gly Asn Ile Lys Gln Gly His Gly Thr Glu Ser Ser Gly
            260                 265                 270
Ser Gly Leu Phe Ala Leu Cys Thr Leu Asp Gly Thr Leu Lys Leu Met
        275                 280                 285
Glu Glu Met Glu Glu Ala Asp Lys Leu Leu Trp Ser Val Gln Val Asp
    290                 295                 300
His Gln Leu Phe Ala Leu Glu Lys Leu Asp Val Thr Gly Asn Gly His
305                 310                 315                 320
Glu Glu Val Val Ala Cys Ala Trp Asp Gly Gln Thr Tyr Ile Ile Asp
                325                 330                 335
His Asn Arg Thr Val Val Arg Phe Gln Val Asp Glu Asn Ile Arg Ala
            340                 345                 350
Phe Cys Ala Gly Leu Tyr Ala Cys Lys Glu Gly Arg Asn Ser Pro Cys
        355                 360                 365
Leu Val Tyr Val Thr Phe Asn Gln Lys Ile Tyr Val Tyr Trp Glu Val
    370                 375                 380
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr
385                 390                 395                 400
Lys Pro Glu Tyr His Ser Leu Leu Gln Glu Leu Gly Val Asp Pro Asp
                405                 410                 415
Asp Leu Pr  Val Thr Arg Ala Leu Leu His Gln Thr Leu Tyr His Pro
            420                 425                 430
Asp Gln Pro Pro Gln Cys Ala Pro Ser Ser Leu Gln Asp Pro Thr
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435 440 445

<210> 66
<211> 1793
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (152)..(760)

<400> 66
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tgactgtttc ttggggcttc atgacagaaa gatgtgtgtt ctcggactct gtgctcttat 180
tgatatggaa cagatacccc aagttttaaa tcaggtttct ggacagattt tgccggcttt 240
tatcctttta tttaacggat tgaaaagagc atatgcctgc catgcagaac atgagaatga 300
cagtgatgat gatgatgaag ctgaagatga tgatgaaacc gaggaactgg ggagtgatga 360
agatgatatt gatgaagatg ggcaagaata tttggagatt ctggctaagc aggctggtga 420
agatggagat gatgaagatt gggaagaaga tgatgctgaa gagactgctc tggaaggcta 480
ttccacaatc attgatgatg aagataaccc tgttgatgag tatcagatat ttaaagctat 540
ctttcaaact attcaaaatc gtaatcctgt gtggtatcag gcactgactc acggtcttaa 600
tgaagaacaa agaaaacagt tacaggacat agcaactctg gctgatcaaa gaagagcagc 660
ccatgaatcc aaaatgattg agaagcatgg aggatacaaa ttcagtgctc cagttgtgcc 720
aagttctttc aattttggag gcccagcacc agggatgaat tgagttatct ctttctttcc 780
tgctgtgtgc ttgtagtgaa gagcttgtgt tcctcctagt agtggttcca gaactggttc 840
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taaagctgtc agtgtacaag tgggtatttg aataccagac cttactgtaa aaaataaaaa 1680
aggtggtatc tagagcatgt aaattggata taaagttctg ctcttaaaga gttgatctaa 1740
gagtatggct aaacatctat atatgcaatc tattaaaaga acttaattcg gct 1793

<210> 67
<211> 203
<212> PRT

<213> Homo sapiens

<400> 67

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Met Cys Val Leu Gly Leu Cys Ala Leu Ile Asp Met Glu Gln Ile Pro
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Gln Val Leu Asn Gln Val Ser Gly Gln Ile Leu Pro Ala Phe Ile Leu
            20                  25                  30
Leu Phe Asn Gly Leu Lys Arg Ala Tyr Ala Cys His Ala Glu His Glu
        35                  40                  45
Asn Asp Ser Asp Asp Asp Asp Glu Ala Glu Asp Asp Asp Glu Thr Glu
    50                  55                  60
Glu Leu Gly Ser Asp Glu Asp Asp Ile Asp Glu Asp Gly Gln Glu Tyr
65                  70                  75                  80
Leu Glu Ile Leu Ala Lys Gln Ala Gly Glu Asp Gly Asp Asp Glu Asp
                85                  90                  95
Trp Glu Glu Asp Asp Ala Glu Glu Thr Ala Leu Glu Gly Tyr Ser Thr
            100                 105                 110
Ile Ile Asp Asp Glu Asp Asn Pro Val Asp Glu Tyr Gln Ile Phe Lys
        115                 120                 125
Ala Ile Phe Gln Thr Ile Gln Asn Arg Asn Pro Val Trp Tyr Gln Ala
    130                 135                 140
Leu Thr His Gly Leu Asn Glu Glu Gln Arg Lys Gln Leu Gln Asp Ile
145                 150                 155                 160
Ala Thr Leu Ala Asp Gln Arg Arg Ala Ala His Glu Ser Lys Met Ile
                165                 170                 175
Glu Lys His Gly Gly Tyr Lys Phe Ser Ala Pro Val Val Pro Ser Ser
            180                 185                 190
Phe Asn Phe Gly Gly Pro Ala Pro Gly Met Asn
        195                 200
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<210> 68
<211> 2160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (115)..(1146)

<400> 68

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atgaagttat ttcagaccat ttgcaggcag ctcaggagtt caaagtttc tgtggaatca 180
gctgcccttg tggctttctc tacttcctct tactcatgtg gccggaagaa aaaagtgaac 240
ccatatgaag aagtggacca agaaaaatac tctaatttag ttcagtctgt cttgtcatcc 300
agaggcgtcg cccagacccc gggatcggtg gaggaagatg ctttgctctg tggacccgtg 360
agcaagcata agctgccaaa ccaaggtgag gacagacgag tgccacaaaa ctggtttcct 420
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atccccttgc aaaggaatgt gataccaagt gtgacccgag tccttcagca gaccatgaca 540
aaacaacagg ttttcttgtt ggagaggtgg aaacagcgga tgattctgga actgggagaa 600
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ttggaaagca tactttcacc ccaggaaacc ttaaaagaga gagatgaaaa tctcctcaag 720
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caaagtacat ttgacaaccc actgcaagtt gtggcataca tgggtgccat gaaccatgat 960
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tcagaatagg gagcaagttg ctatttggga acattcagca ccttctcaca gtttggtaac 1200
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<210> 69
<211> 344
<212> PRT
<213> Homo sapiens

<400> 69
Met Lys Met Lys Leu Phe Gln Thr Ile Cys Arg Gln Leu Arg Ser Ser
1 5 10 15
Lys Phe Ser Val Glu Ser Ala Ala Leu Val Ala Phe Ser Thr Ser Ser
20 25 30
Tyr Ser Cys Gly Arg Lys Lys Lys Val Asn Pro Tyr Glu Glu Val Asp
35 40 45
Gln Glu Lys Tyr Ser Asn Leu Val Gln Ser Val Leu Ser Ser Arg Gly
50 55 60
Val Ala Gln Thr Pro Gly Ser Val Glu Glu Asp Ala Leu Leu Cys Gly
65 70 75 80
Pro Val Ser Lys His Lys Leu Pro Asn Gln Gly Glu Asp Arg Arg Val

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                85                  90                  95
Pro Gln Asn Trp Phe Pro Ile Phe Asn Pro Glu Arg Ser Asp Lys Pro
            100                 105                 110
Asn Ala Ser Asp Pro Ser Val Pro Leu Lys Ile Pro Leu Gln Arg Asn
        115                 120                 125
Val Ile Pro Ser Val Thr Arg Val Leu Gln Gln Thr Met Thr Lys Gln
    130                 135                 140
Gln Val Phe Leu Leu Glu Arg Trp Lys Gln Arg Met Ile Leu Glu Leu
145                 150                 155                 160
Gly Glu Asp Gly Phe Lys Glu Tyr Thr Ser Asn Val Phe Leu Gln Gly
                165                 170                 175
Lys Arg Phe His Glu Ala Leu Glu Ser Ile Leu Ser Pro Gln Glu Thr
            180                 185                 190
Leu Lys Glu Arg Asp Glu Asn Leu Leu Lys Ser Gly Tyr Ile Glu Ser
        195                 200                 205
Val Gln His Ile Leu Lys Asp Val Ser Gly Val Arg Ala Leu Glu Ser
    210                 215                 220
Ala Val Gln His Glu Thr Leu Asn Tyr Ile Gly Leu Leu Asp Cys Val
225                 230                 235                 240
Ala Glu Tyr Gln Gly Lys Leu Cys Val Ile Asp Trp Lys Thr Ser Glu
                245                 250                 255
Lys Pro Lys Pro Phe Ile Gln Ser Thr Phe Asp Asn Pro Leu Gln Val
            260                 265                 270
Val Ala Tyr Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln
        275                 280                 285
Val Gln Cys Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala
    290                 295                 300
His Pro His Leu Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys
305                 310                 315                 320
Trp Leu Leu Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn
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Ile Gln Lys Pro Glu Tyr Ser Glu
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<210> 70
<211> 1998
<212> DNA
<213> Homo sapiens

<400> 70

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ccttttgaaa taagtgcaga tatttattta accctccctt ccccaccctc tgccccactt 360
ccagccctct gaaagattgg agtcaagcag atggaagaat gcagtggtga tagttgtcat 420
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ccacatcccc taacatctga ttcacgactt aatgtatgtt gtaagaaaag aaaaaagaaa 1920
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<210> 71
<211> 1763
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (540)..(1529)

<400> 71
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aagtccatgt ggctcttcac agtgaatcag gtgttaagga agatgcagag acgccacagc 240
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<210> 72
<211> 330
<212> PRT
<213> Homo sapiens

<400> 72
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35 40 45
Glu Glu Gly Gly Asp Glu Gln Pro Gly Thr Pro Ala Pro Ala Leu Ser
50 55 60
Glu Leu Lys Ala Val Ile Cys Trp Leu Gln Lys Gly Leu Pro Phe Ile
65 70 75 80
Leu Ile Leu Leu Ala Lys Leu Cys Phe Gln His Lys Leu Gly Ile Ala
85 90 95
Val Cys Ile Gly Met Ala Ser Thr Phe Ala Tyr Ala Asn Ser Thr Leu
100 105 110
Arg Glu Gln Val Ser Leu Lys Glu Lys Arg Ser Val Leu Val Ile Leu
115 120 125
Trp Ile L u Ala Phe Leu Ala Gly Asn Thr Leu Tyr Val Leu Tyr Thr
130 135 140
Phe Ser S r Gln Gln Leu Tyr Asn Ser Leu Ile Phe Leu Lys Pro Asn

145 150 155 160
Leu Glu Met Leu Asp Phe Phe Asp Leu Leu Trp Ile Val Gly Ile Ala
165 170 175
Asp Phe Val Leu Lys Tyr Ile Thr Ile Ala Leu Lys Cys Leu Ile Val
180 185 190
Ala Leu Pro Lys Ile Ile Leu Ala Val Lys Ser Lys Gly Lys Phe Tyr
195 200 205
Leu Val Ile Glu Glu Leu Ser Gln Leu Phe Arg Ser Leu Val Pro Ile
210 215 220
Gln Leu Trp Tyr Lys Tyr Ile Met Gly Asp Asp Ser Ser Asn Ser Tyr
225 230 235 240
Phe Leu Gly Gly Val Leu Ile Val Leu Tyr Ser Leu Cys Lys Ser Phe
245 250 255
Asp Ile Cys Gly Arg Val Gly Gly Val Arg Lys Ala Leu Lys Leu Leu
260 265 270
Cys Thr Ser Gln Asn Tyr Gly Val Arg Ala Thr Gly Gln Gln Cys Thr
275 280 285
Glu Ala Gly Asp Ile Cys Ala Ile Cys Gln Ala Glu Phe Arg Glu Pro
290 295 300
Leu Ile Leu Leu Cys Gln Met Leu Leu Lys Gly His Lys Lys Leu Glu
305 310 315 320
Leu Glu Lys Ile Asp Glu Ser Ala Gly Val
325 330

<210> 73
<211> 3493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40)..(396)

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<210> 74
<211> 119
<212> PRT
<213> Homo sapiens

<400> 74
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20 25 30
Ala Thr Leu Cys Pro Val Glu Ala Arg Arg His Gln Arg Leu Gln Phe
35 40 45
Cys Tyr Ser Leu Leu Gly Met Glu Arg Ser Gly Thr Ala Val Gln Arg
50 55 60
Ser Trp Pro Arg Arg Ser Ser Gly Ile Pro Val Pro Arg Ala Val His
65 70 75 80
Ser Val Ile Leu Arg Leu Pro Gly Val Glu Gly Ile Thr Cys Trp Val
85 90 95
Leu Glu Ser Ile Ala Leu His Leu Arg Lys Glu Lys Ser Gln Lys Asp
100 105 110
Lys Met Thr Cys Pro Arg Ser
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<210> 75
<211> 2654
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (98)..(1027)

<400> 75
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<210> 76
<211> 310
<212> PRT
<213> Homo sapiens

<400> 76
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Arg Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys
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Leu Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr
35 40 45
Lys Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val
50 55 60
Leu Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His

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 65                  70                  75                  80
Phe Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro
                85                  90                  95
Glu Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr
            100                 105                 110
Leu Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu Gln Asn Lys
        115                 120                 125
Asp Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr Ser Ser Lys
    130                 135                 140
Glu Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala Val Lys Leu
145                 150                 155                 160
Leu Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp
                165                 170                 175
Asp Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg
            180                 185                 190
Phe Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile
        195                 200                 205
Cys Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys
    210                 215                 220
Cys Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr Lys Val Glu
225                 230                 235                 240
Phe Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile Leu Leu Tyr
                245                 250                 255
Glu Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu Glu Ala Thr
            260                 265                 270
Gly Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp Glu Glu Arg
        275                 280                 285
Glu Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg Pro Asp Asp
    290                 295                 300
Arg Ala His Leu His Gln
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<210> 77
<211> 2517
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (274)..(687)

<400> 77
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<210> 78
<211> 138
<212> PRT
<213> Homo sapiens

<400> 78
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Ile Asp Cys Val Val Leu Thr Ser Ser Pro Glu Ala Thr Glu Thr Ser
    50                  55                  60
Gln Gln Leu Gln Leu Arg Val Gln Gly Lys Glu Lys His Gln Thr Leu
65                  70                  75                  80
Glu Val Ser Leu Ser Arg Asp Ser Pro Leu Lys Thr Leu Met Ser His
                85                  90                  95
Tyr Glu Glu Ala Met Gly Leu Ser Gly Arg Lys Leu Ser Phe Phe Phe
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Asp Gly Thr Lys Leu Ser Gly Arg Glu Leu Pro Ala Asp Leu Gly Met
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Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
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<210> 79
<211> 2901
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(1974)

<400> 79

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<210> 80
<211> 628
<212> PRT
<213> Homo sapiens

<400> 80

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Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu Lys Ser Ser
         35                  40                  45
Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg
     50                  55                  60
Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu
 65                  70                  75                  80
Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu Ala Pro Ile
                 85                  90                  95
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Pro Pro Thr Leu Leu Ala Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu
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Val Asp Met His Pro Pro Leu Pro Gln Pro Val His Pro Asp Val Thr
115 120 125
Met Lys Pro Leu Pro Phe Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro
130 135 140
Thr Thr Leu Ala Ser Thr Ser Ser Gln Arg Phe Glu Glu Ala His Phe
145 150 155 160
Thr Phe Ala Leu Thr Pro Gln Gln Val Gln Gln Ile Leu Thr Ser Arg
165 170 175
Glu Val Leu Pro Gly Ala Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu
180 185 190
Arg Phe Cys Leu Cys Glu Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro
195 200 205
Pro Asn Leu Phe Val Lys Val Asn Gly Lys Leu Cys Pro Leu Pro Gly
210 215 220
Tyr Leu Pro Pro Thr Lys Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg
225 230 235 240
Pro Ile Asn Ile Thr Pro Pro Ala Arg Leu Ser Ala Thr Val Pro Asn
245 250 255
Thr Ile Val Val Asn Trp Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu
260 265 270
Ser Val Tyr Leu Val Arg Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys
275 280 285
Leu Arg Ala Lys Gly Ile Arg Asn Pro Asp His Ser Arg Ala Leu Ile
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Lys Glu Lys Leu Thr Ala Asp Pro Asp Ser Glu Val Ala Thr Thr Ser
305 310 315 320
Leu Arg Val Ser Leu Met Cys Pro Leu Gly Lys Met Arg Leu Thr Val
325 330 335
Pro Cys Arg Ala Leu Thr Cys Ala His Leu Gln Ser Phe Asp Ala Ala
340 345 350
Leu Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Thr Cys Pro Val
355 360 365
Cys Asp Lys Lys Ala Pro Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe
370 375 380
Met Glu Ile Leu Ser Ser Cys Ser Asp Cys Asp Glu Ile Gln Phe Met
385 390 395 400
Glu Asp Gly Ser Trp Cys Pro Met Lys Pro Lys Lys Glu Ala Ser Glu
405 410 415
Val Cys Pro Pro Pro Gly Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro
420 425 430
Val Gln Gly Gly Asp Pro Ser Glu Asn Lys Lys Lys Val Glu Val Ile
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Asp Leu Thr Ile Glu Ser Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr
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Lys Lys His Cys Ser Val Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly
465 470 475 480

Ser Lys Gly Val Leu Thr Ser Gly His Gln Pro Ser Ser Val Leu Arg
485 490 495
Ser Pro Ala Met Gly Thr Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro
500 505 510
Leu His Glu Tyr Pro Pro Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly
515 520 525
Leu Asp Leu Phe Ser Phe Leu Gln Thr Glu Ser Gln His Tyr Gly Pro
530 535 540
Ser Val Ile Thr Ser Leu Asp Glu Gln Asp Ala Leu Gly His Phe Phe
545 550 555 560
Gln Tyr Arg Gly Thr Pro Ser His Phe Leu Gly Pro Leu Ala Pro Thr
565 570 575
Leu Gly Ser Ser His Cys Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg
580 585 590
Val Ser Ser Ile Val Ala Pro Gly Gly Ala Leu Arg Glu Gly His Gly
595 600 605
Gly Pro Leu Pro Ser Gly Pro Ser Leu Thr Gly Cys Arg Ser Asp Ile
610 615 620
Ile Ser Leu Asp
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<210> 81
<211> 2130
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (186)..(1262)

<400> 81
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<210> 82
<211> 359
<212> PRT
<213> Homo sapiens

<400> 82
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35 40 45
Ser Leu Pro Cys Lys His Val Phe Cys Tyr Leu Cys Val Lys Gly Ala
50 55 60
Ser Trp Leu Gly Lys Arg Cys Ala Leu Cys Arg Gln Glu Ile Pro Glu
65 70 75 80
Asp Phe Leu Asp Lys Pro Thr Leu Leu Ser Pro Glu Glu Leu Lys Ala
85 90 95
Ala Ser Arg Gly Asn Gly Glu Tyr Ala Trp Tyr Tyr Glu Gly Arg Asn
100 105 110
Gly Trp Trp Gln Tyr Asp Glu Arg Thr Ser Arg Glu Leu Glu Asp Ala
115 120 125
Phe S r Lys Gly Lys Lys Asn Thr Glu Met Leu Ile Ala Gly Phe Leu
130 135 140
Tyr Val Ala Asp Leu Glu Asn Met Val Gln Tyr Arg Arg Asn Glu His
145 150 155 160

Gly Arg Arg Arg Lys Ile Lys Arg Asp Ile Ile Asp Ile Pro Lys Lys
165 170 175
Gly Val Ala Gly Leu Arg Leu Asp Cys Asp Ala Asn Thr Val Asn Leu
180 185 190
Ala Arg Glu Ser Ser Ala Asp Gly Ala Asp Ser Val Ser Ala Gln Ser
195 200 205
Gly Ala Ser Val Gln Pro Leu Val Ser Ser Val Arg Pro Leu Thr Ser
210 215 220
Val Asp Gly Gln Leu Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser
225 230 235 240
Thr Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn
245 250 255
Thr Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser
260 265 270
Pro Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr
275 280 285
Glu Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala
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Gln His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln
305 310 315 320
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<210> 83
<211> 2748
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (250)..(1011)

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<210> 84
<211> 254
<212> PRT
<213> Homo sapiens

<400> 84
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Lys Glu Ala Gln Gly Lys Ile Asp Val Leu Gln Ala Glu Val Ala Ala
20 25 30

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Pro Leu Pro Gly Gly Lys Thr Pro Phe Lys Lys Gly His Thr Arg Asn
      50                  55                  60
Lys Ser Thr Ser Ser Ala Met Ser Gly Ser His Gln Asp Leu Ser Val
 65                  70                  75                  80
Ile Gln Pro Ile Val Lys Asp Cys Lys Glu Ala Asp Leu Ser Leu Tyr
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Asn Glu Phe Arg Leu Trp Lys Asp Glu Pro Thr Met Asp Arg Thr Cys
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Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr
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Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
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Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
145                 150                 155                 160
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
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Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
            180                 185                 190
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
        195                 200                 205
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
    210                 215                 220
Gln Gln Asp Val Asp Gln Met Phe Trp Glu Val Met Gln Leu Arg Lys
225                 230                 235                 240
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (265)..(2031)

<400> 85

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<211> 589
<212> PRT
<213> Homo sapiens

<400> 86

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        35                  40                  45
Glu Phe Ala Val Pro Glu Asn Ser Ser Val Gln Gln Phe Lys Glu Glu
    50                  55                  60
Ile Ser Lys Arg Phe Lys Ser His Thr Asp Gln Leu Val Leu Ile Phe
65                  70                  75                  80
Ala Gly Lys Ile Leu Lys Asp Gln Asp Thr Leu Ser Gln His Gly Ile
                85                  90                  95
His Asp Gly Leu Thr Val His Leu Val Ile Lys Thr Gln Asn Arg Pro
            100                 105                 110
Gln Asp His Ser Ala Gln Gln Thr Asn Thr Ala Gly Ser Asn Val Thr
        115                 120                 125
Thr Ser Ser Thr Pro Asn Ser Asn Ser Thr Ser Gly Ser Ala Thr Ser
    130                 135                 140
Asn Pro Phe Gly Leu Gly Gly Leu Gly Gly Leu Ala Gly Leu Ser Ser
145                 150                 155                 160
Leu Gly Leu Asn Thr Thr Asn Phe Ser Glu Leu Gln Ser Gln Met Gln
                165                 170                 175
Arg Gln Leu Leu Ser Asn Pro Glu Met Met Val Gln Ile Met Glu Asn
            180                 185                 190
Pro Phe Val Gln Ser Met Leu Ser Asn Pro Asp Leu Met Arg Gln Leu
        195                 200                 205
Ile Met Ala Asn Pro Gln Met Gln Gln Leu Ile Gln Arg Asn Pro Glu
    210                 215                 220
Ile Ser His Met Leu Asn Asn Pro Asp Ile Met Arg Gln Thr Leu Glu
225                 230                 235                 240
Leu Ala Arg Asn Pro Ala Met Met Gln Glu Met Met Arg Asn Gln Asp
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Arg Ala Leu Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Ala Leu
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Arg Arg Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala Gln
        275                 280                 285
Glu Gln Phe Gly Gly Asn Pro Phe Ala Ser Leu Val Ser Asn Thr Ser
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Ser Gly Glu Gly Ser Gln Pro Ser Arg Thr Glu Asn Arg Asp Pro Leu
305                 310                 315                 320
Pro Asn Pro Trp Ala Pro Gln Thr Ser Gln Ser Ser Ser Ala Ser Ser
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Gly Thr Ala Ser Thr Val Gly Gly Thr Thr Gly Ser Thr Ala Ser Gly
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Thr Ser Gly Gln Ser Thr Thr Ala Pro Asn Leu Val Pro Gly Val Gly
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Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro Asp Leu Ala Ala Gln
405 410 415
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420 425 430
Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln Met Arg Asn Pro
435 440 445
Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met Gln Ala Leu Leu
450 455 460
Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr Glu Ala Pro Gly Leu
465 470 475 480
Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly Ser Thr Gly Gly
485 490 495
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500 505 510
Pro Thr Ala Gly Thr Thr Glu Pro Gly His Gln Gln Phe Ile Gln Gln
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<212> DNA
<213> Homo sapiens

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<222> (197)..(496)

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<211> 100
<212> PRT
<213> Homo sapiens

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35 40 45
Ala Asp Ser Leu Thr Ser Leu Arg Lys Leu Ala Glu Gln Phe Pro Arg
50 55 60
Gln Val Leu Asp Ser Lys Ala Pro Lys Pro Glu Asp Ile Asp Glu Glu
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85 90 95

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<210> 89
<211> 2551
<212> DNA
<213> Homo sapiens

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<222> (42)..(1883)

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<210> 90
<211> 614
<212> PRT
<213> Homo sapiens

<400> 90

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			20					25					30		
Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg	Glu	Leu	Pro
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Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn	Tyr	Arg	Asp
	50					55					60				
Met	Gly	Glu	His	Arg	Val	Ile	Leu	Pro	Asp	Asp	Val	Arg	Asp	Phe	Ile
65					70					75					80
Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe	Arg	Tyr	Ala	Glu
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Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala	Asn	Gly	Gln
				165					170					175	
Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Val	Pro	Ala	Gly	Ala	Val
			180					185					190		
Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala	Pro	Gln	Leu
		195					200					205			
Pro	Leu	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val	Pro	Pro	Ser
	210					215					220				
Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala	Pro	Arg	Arg
225					230					235					240
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Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val Gly Ala Lys
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Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu Gly Gly Asn
305                 310                 315                 320
Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu Asp Gln Pro
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Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser Gln Asp Ile
            340                 345                 350
Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro Thr Lys Gly
        355                 360                 365
Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr Lys Trp Ser
    370                 375                 380
Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro Thr Arg Thr
385                 390                 395                 400
Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr Gly Pro Glu
                405                 410                 415
Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro Gly Lys Gly
            420                 425                 430
Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro Ile Ala Ala
        435                 440                 445
Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu Ser Glu Gly
    450                 455                 460
Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg Asp Asp Pro
465                 470                 475                 480
Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro Pro Pro Pro
                485                 490                 495
Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp Ser Asp Leu
            500                 505                 510
Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser Ser Glu Glu
        515                 520                 525
Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys Lys Lys Lys
    530                 535                 540
Lys Gly Lys Glu Glu Glu Glu Lys Ala Ala Lys Lys Lys Ser Lys His
545                 550                 555                 560
Lys Lys Ser Lys Asp Lys Glu Glu Gly Lys Glu Glu Arg Arg Arg Arg
                565                 570                 575
Gln Gln Arg Pro Pro Arg Ser Arg Glu Arg Thr Ala Ala Asp Glu Leu
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Gly Asp Tyr Glu Glu Leu
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<210> 91
<211> 3133
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (113)..(1879)

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<222> (145)..(1926)

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<400> 94

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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

<400> 96

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Asp	Met	Thr	Pro	Leu	Asn	Leu	Ser	Ser	Arg	Ala	Glu	Pro	Val	Arg	Asp
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Ser	Ser	His	Ala	Arg	Ser	His	Leu	Arg	Gln	Met	Gly	Val	Thr	Glu	Trp
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Pro	Gly	Ala	Gly	Pro	Ala	Gln	Val	Pro	Arg	Glu	Leu	Ser	Leu	Thr	Pro
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Ala	Lys	Arg	Pro	Leu	Gln	Glu	Asp	Arg	Leu	Leu	Pro	Ala	Glu	Val	Lys
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His	Glu	Lys	Thr	Ser	His	Ser	Ser	Thr	Glu	Ala	Cys	Cys	Glu	Leu	Cys

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245 250 255
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260 265 270
Ile Glu Thr Leu Ser Glu Trp Ile Lys His Arg Pro Gln Lys Val Gly
275 280 285
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325 330 335
Pro Gly Pro Glu Ala Gly Arg Ala Ala Asp Gly Gly Glu Arg Pro Leu
340 345 350
Ala Ala Ser Pro Pro Gly Thr Val Lys Ala Glu Glu His Gln Arg Gln
355 360 365
Asn Ile Asn Lys Phe Glu Arg Arg Gln Ala Arg Pro Pro Asp Ala Ser
370 375 380
Ala Ala Arg Gly Gly Glu Asp Thr Asn Asp Leu Gln Gln Lys Leu Glu
385 390 395 400
Glu Val Arg Gln Pro Pro Pro Arg Val Arg Pro Val Pro Ser Leu Val
405 410 415
Pro Arg Pro Pro Gln Thr Ser Leu Val Lys Phe Val Gly Asn Ile Tyr
420 425 430
Thr Leu Lys Cys Arg Phe Cys Glu Val Glu Phe Gln Gly Pro Leu Ser
435 440 445
Ile Gln Glu Glu Trp Val Arg His Leu Gln Arg His Ile Leu Glu Met
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<400> 98

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Asp Glu Glu Thr Val Ala Glu Ile Asn Ala Thr Met Ser Val His Leu
     50                  55                  60
Pro Phe Ala Val Val Gly Ser Thr Glu Glu Val Lys Ile Gly Asn Lys
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Met Ala Lys Ala Arg Gln Tyr Pro Trp Gly Val Val Gln Val Glu Asn
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Glu Asn His Cys Asp Phe Val Lys Leu Arg Glu Met Leu Ile Arg Val
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Asn Met Glu Asp Leu Arg Glu Gln Thr His Thr Arg His Tyr Glu Leu
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Tyr Arg Arg Cys Lys Leu Glu Glu Met Gly Phe Lys Asp Thr Asp Pro
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Asp Ser Lys Pro Phe Ser Leu Gln Glu Thr Tyr Glu Ala Lys Arg Asn
145                 150                 155                 160
Glu Phe Leu Gly Glu Leu Gln Lys Lys Glu Glu Glu Met Arg Gln Met
                165                 170                 175
Phe Val Met Arg Val Lys Glu Lys Glu Ala Glu Leu Lys Glu Ala Glu
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Lys Glu Leu His Glu Lys Phe Asp Leu Leu Lys Arg Thr His Gln Glu
        195                 200                 205
Glu Lys Lys Lys Val Glu Asp Lys Lys Lys Glu Leu Glu Glu Glu Val
    210                 215                 220
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Asn Asn Phe Gln Lys Lys Lys Ala Ala Ala Gln Leu Leu Gln Ser Gln
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<212> PRT
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Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr
50 55 60
Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro
65 70 75 80
Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser
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Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly

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Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr
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Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr Leu Pro Gln Ser Ser
145                 150                 155                 160
Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg Ser Leu Lys Thr Gln
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Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp Pro Leu Arg Lys Ser
            180                 185                 190
Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser Ala His Leu Pro Ala
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Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser Thr Arg Pro Leu Pro
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Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu His Arg Gln Ala Glu
225                 230                 235                 240
Val His Lys Val Ser Arg Pro Glu Asn Glu Gln Leu Arg Asn Asp Asn
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Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala Pro Arg Arg Gly Arg
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Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly Ile Arg Arg Asp Gly
        275                 280                 285
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Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His Asn Lys Leu Lys Leu
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Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro Val Asn Gly Glu Asp
                325                 330                 335
Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser Glu Gly Asn Ala Asp
            340                 345                 350
Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr Asp Lys Thr Lys Ser
        355                 360                 365
Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg Glu Arg Arg Pro Thr
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Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr Phe Gly Ile Pro Leu
385                 390                 395                 400
Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Leu Gly
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Phe Arg Gly Gly Arg Gly Arg Gly Gly Gly Arg Gly Gly Thr Phe Thr
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<211> 2284
<212> DNA
<213> Homo sapiens

<220>
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<222> (128)..(1936)

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<210> 102
<211> 603
<212> PRT
<213> Homo sapiens

<400> 102

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         35                  40                  45
Met Asp Trp Gln Ser Ile Lys Ile Gln Glu Leu Met Ser Asp Asp Gln
     50                  55                  60
Arg Glu Ala Gly Arg Ile Pro Arg Thr Ile Glu Cys Glu Leu Val His
 65                  70                  75                  80
Asp Leu Val Asp Ser Cys Val Pro Gly Asp Thr Val Thr Ile Thr Gly
                 85                  90                  95
Ile Val Lys Val Ser Asn Ala Glu Glu Gly Ser Arg Asn Lys Asn Asp
            100                 105                 110
Lys Cys Met Phe Leu Leu Tyr Ile Glu Ala Asn Ser Ile Ser Asn Ser
        115                 120                 125
Lys Gly Gln Lys Thr Lys Ser Ser Glu Asp Gly Cys Lys His Gly Met
    130                 135                 140
Leu Met Glu Phe Ser Leu Lys Asp Leu Tyr Ala Ile Gln Glu Ile Gln
145                 150                 155                 160
Ala Glu Glu Asn Leu Phe Lys Leu Ile Val Asn Ser Leu Cys Pro Val
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Gly Gly Ser Gln Lys Tyr Ala Asp Asp Lys Asn Arg Ile Pro Ile Arg
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Gly Asp Pro His Ile Leu Val Val Gly Asp Pro Gly Leu Gly Lys Ser
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Gln Met Leu Gln Ala Ala Cys Asn Val Ala Pro Arg Gly Val Tyr Val
225                 230                 235                 240
Cys Gly Asn Thr Thr Thr Thr Ser Gly Leu Thr Val Thr Leu Ser Lys
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Asp Ser Ser Ser Gly Asp Phe Ala Leu Glu Ala Gly Ala Leu Val Leu
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Gly Asp Gln Gly Ile Cys Gly Ile Asp Glu Phe Asp Lys Met Gly Asn
        275                 280                 285
Gln His Gln Ala Leu Leu Glu Ala Met Glu Gln Gln Ser Ile Ser Leu
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Ser Glu His Val Ile Ala Ile Arg Ala Gly Lys Gln Arg Thr Ile Ser
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Ser Ala Thr Val Ala Arg Met Asn Ser Gln Asp Ser Asn Thr Ser Val
385 390 395 400
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405 410 415
Pro Gly Glu Thr Ile Asp Pro Ile Pro His Gln Leu Leu Arg Lys Tyr
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Ile Gly Tyr Ala Arg Gln Tyr Val Tyr Pro Arg Leu Ser Thr Glu Ala
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Ala Arg Val Leu Gln Asp Phe Tyr Leu Glu Leu Arg Lys Gln Ser Gln
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Arg Leu Thr Glu Ala Arg Ala Arg Leu Glu Leu Arg Glu Glu Ala Thr
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Lys Glu Asp Ala Glu Asp Ile Val Glu Ile Met Lys Tyr Ser Met Leu
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (725)..(1513)

<400> 103

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<210> 104
<211> 263
<212> PRT
<213> Homo sapiens

<400> 104

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         35                  40                  45
Ile Asn Ala Lys Arg Val Tyr Arg Ile Met Arg Gln Asn Ala Leu Leu
     50                  55                  60
Leu Glu Arg Lys Pro Ala Val Pro Pro Ser Lys Arg Ala His Thr Gly
 65                  70                  75                  80
Arg Val Ala Val Lys Glu Ser Asn Gln Arg Trp Cys Ser Asp Gly Phe
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Glu Phe Cys Cys Asp Asn Gly Glu Arg Leu Arg Val Thr Phe Ala Leu
            100                 105                 110
Asp Cys Cys Asp Arg Glu Ala Leu His Trp Ala Val Thr Thr Gly Gly
        115                 120                 125
Phe Asn Ser Glu Thr Val Gln Asp Val Met Leu Gly Ala Val Glu Arg
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Arg Phe Gly Asn Asp Leu Pro Ser Ser Pro Val Glu Trp Leu Thr Asp
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Asn Gly Ser Cys Tyr Arg Ala Asn Glu Thr Arg Gln Phe Ala Arg Met
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Leu Gly Leu Glu Pro Lys Asn Thr Ala Val Arg Ser Pro Glu Ser Asn
            180                 185                 190
Gly Ile Ala Glu Ser Phe Val Lys Thr Ile Lys Arg Asp Tyr Ile Ser
        195                 200                 205
Ile Met Pro Lys Pro Asp Gly Leu Thr Ala Ala Lys Asn Leu Ala Glu
    210                 215                 220
Ala Phe Glu His Tyr Asn Glu Trp His Pro His Ser Ala Leu Gly Tyr
225                 230                 235                 240
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<211> 3338
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (201)..(1904)

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<210> 106
<211> 568
<212> PRT
<213> Homo sapiens

<400> 106

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Cys Asp Val Thr Leu Arg Val Glu Gln Lys Asp Phe Pro Ala His Arg
         35                  40                  45
Ile Val Leu Ala Ala Cys Ser Asp Tyr Phe Cys Ala Met Phe Thr Ser
     50                  55                  60
Glu Leu Ser Glu Lys Gly Lys Pro Tyr Val Asp Ile Gln Gly Leu Thr
 65                  70                  75                  80
Ala Ser Thr Met Glu Ile Leu Leu Asp Phe Val Tyr Thr Glu Thr Val
                 85                  90                  95
His Val Thr Val Glu Asn Val Gln Glu Leu Leu Pro Ala Ala Cys Leu
            100                 105                 110
Leu Gln Leu Lys Gly Val Lys Gln Ala Cys Cys Glu Phe Leu Glu Ser
        115                 120                 125
Gln L u Asp Pro Ser Asn Cys Leu Gly Ile Arg Asp Phe Ala Glu Thr
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His Asn Cys Val Asp Leu Met Gln Ala Ala Glu Val Phe Ser Gln Lys
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His Phe Pro Glu Val Val Gln His Glu Glu Phe Ile Leu Leu Ser Gln
                165                 170                 175
Gly Glu Val Glu Lys Leu Ile Lys Cys Asp Glu Ile Gln Val Asp Ser
            180                 185                 190
Glu Glu Pro Val Phe Glu Ala Val Ile Asn Trp Val Lys His Ala Lys
        195                 200                 205
Lys Glu Arg Glu Glu Ser Leu Pro Asn Leu Leu Gln Tyr Val Arg Met
    210                 215                 220
Pro Leu Leu Thr Pro Arg Tyr Ile Thr Asp Val Ile Asp Ala Glu Pro
225                 230                 235                 240
Phe Ile Arg Cys Ser Leu Gln Cys Arg Asp Leu Val Asp Glu Ala Lys
                245                 250                 255
Lys Phe His Leu Arg Pro Glu Leu Arg Ser Gln Met Gln Gly Pro Arg
            260                 265                 270
Thr Arg Ala Arg Leu Gly Ala Asn Glu Val Leu Leu Val Val Gly Gly
        275                 280                 285
Phe Gly Ser Gln Gln Ser Pro Ile Asp Val Val Glu Lys Tyr Asp Pro
    290                 295                 300
Lys Thr Gln Glu Trp Ser Phe Leu Pro Ser Ile Thr Arg Lys Arg Arg
305                 310                 315                 320
Tyr Val Ala Ser Val Ser Leu His Asp Arg Ile Tyr Val Ile Gly Gly
                325                 330                 335
Tyr Asp Gly Arg Ser Arg Leu Ser Ser Val Glu Cys Leu Asp Tyr Thr
            340                 345                 350
Ala Asp Glu Asp Gly Val Trp Tyr Ser Val Ala Pro Met Asn Val Arg
        355                 360                 365
Arg Gly Leu Ala Gly Ala Thr Thr Leu Gly Asp Met Ile Tyr Val Ser
    370                 375                 380
Gly Gly Phe Asp Gly Ser Arg Arg His Thr Ser Met Glu Arg Tyr Asp
385                 390                 395                 400
Pro Asn Ile Asp Gln Trp Ser Met Leu Gly Asp Met Gln Thr Ala Arg
                405                 410                 415
Glu Gly Ala Gly Leu Val Val Ala Ser Gly Val Ile Tyr Cys Leu Gly
            420                 425                 430
Gly Tyr Asp Gly Leu Asn Ile Leu Asn Ser Val Glu Lys Tyr Asp Pro
        435                 440                 445
His Thr Gly His Trp Thr Asn Val Thr Pro Met Ala Thr Lys Arg Ser
    450                 455                 460
Gly Ala Gly Val Ala Leu Leu Asn Asp His Ile Tyr Val Val Gly Gly
465                 470                 475                 480
Phe Asp Gly Thr Ala His Leu Ser Ser Val Glu Ala Tyr Asn Ile Arg
                485                 490                 495
Thr Asp Ser Trp Thr Thr Val Thr Ser Met Thr Thr Pro Arg Cys Tyr
            500                 505                 510
Val Gly Ala Thr Val Leu Arg Gly Arg Leu Tyr Ala Ile Ala Gly Tyr
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Gly Val Cys Val Leu Arg Glu Lys
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<211> 2925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (72)..(1160)

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<212> PRT
<213> Homo sapiens

<400> 108

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Ser Ser Ser Leu Gly Ser Gly Glu Ser Pro Phe Ser Arg Ser Val Thr
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            100                 105                 110
Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr
        115                 120                 125
Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
    130                 135                 140
Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
145                 150                 155                 160
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
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Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
            180                 185                 190
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
        195                 200                 205
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
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<400> 111

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<212> PRT
<213> Homo sapiens

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Asn Phe Pro Arg Leu Asn Arg Arg Leu Leu Gln Gln Ser Gly Ala Gln
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Gln Phe Arg Met Arg Val Arg Trp Gly Ile Gln Gln Asn Ser Gly Phe
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Gly Lys Thr Ser Leu Asn His Arg Gly Arg Val Met Pro Gly Lys Arg
85 90 95
Arg Pro Asn Gly Val Ile Thr Gly Leu Ala Ala Arg Lys Thr Thr Gly
100 105 110
Ile Arg Lys Gly Ile Ser Pro Met Asn Arg Pro Pro Leu Ser Asp Lys
115 120 125
Asn Ile Glu Gln Tyr Phe Pro Val Leu Lys Arg Lys Ala Asn Leu Leu
130 135 140
Arg Gln Asn Glu Gly Gln Arg Lys Pro Val Ala Val Leu Lys Arg Pro
145 150 155 160
Ser Gln Leu Ser Arg Lys Asn Asn Ile Pro Ala Asn Phe Thr Arg Ser
165 170 175
Gly Asn Lys Leu Asn His Gln Lys Asp Thr Arg Gln Ala Thr Phe Leu
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Phe Arg Arg Gly Leu Lys Val Gln Ala Gln Leu Asn Thr Glu Gln Leu
195 200 205
Leu Asp Asp Val Val Ala Lys Arg Thr Arg Gln Trp Arg Thr Ser Thr
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Thr Asn Gly Gly Ile Leu Thr Val Ser Ile Asp Asn Pro Gly Ala Val
225 230 235 240
Gln Cys Pro Val Thr Gln Lys Pro Arg Leu Thr Arg Thr Ala Val Pro
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Ser Phe Leu Thr Lys Arg Gly Gln Ser Asp Val Lys Lys Val Pro Lys
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Gly Val Pro Leu Gln Phe Asp Ile Asn Ser Val Gly Lys Gln Thr Gly
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<212> DNA
<213> Homo sapiens

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<210> 114
<211> 793
<212> PRT
<213> Homo sapiens

<400> 114

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         35                  40                  45
Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu Lys Leu His Pro
     50                  55                  60
Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly Asp Phe Leu Lys Ile
 65                  70                  75                  80
Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu Asp Leu Arg Lys Lys Tyr
                 85                  90                  95
Asp Lys Tyr Gly Glu Lys Gly Leu Glu Asp Asn Gln Gly Gly Gln Tyr
            100                 105                 110
Glu Ser Trp Asn Tyr Tyr Arg Tyr Asp Phe Gly Ile Tyr Asp Asp Asp
        115                 120                 125
Pro Glu Ile Ile Thr Leu Glu Arg Arg Glu Phe Asp Ala Ala Val Asn
    130                 135                 140
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Ser Gly Glu Leu Trp Phe Val Asn Phe Tyr Ser Pro Gly Cys Ser His
145 150 155 160
Cys His Asp Leu Ala Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp
165 170 175
Gly Leu Leu Arg Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu
180 185 190
Cys Arg Met Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg
195 200 205
Ser Gly Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser
210 215 220
Leu Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu
225 230 235 240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala Gly
245 250 255
Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys Leu Thr
260 265 270
Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Asp Gly Leu Val Asn
275 280 285
Val Gly Trp Met Asp Cys Ala Thr Gln Asp Asn Leu Cys Lys Ser Leu
290 295 300
Asp Ile Thr Thr Ser Thr Thr Ala Tyr Phe Pro Pro Gly Ala Thr Leu
305 310 315 320
Asn Asn Lys Glu Lys Asn Ser Ile Leu Phe Leu Asn Ser Leu Asp Ala
325 330 335
Lys Glu Ile Tyr Leu Glu Val Ile His Asn Leu Pro Asp Phe Glu Leu
340 345 350
Leu Ser Ala Asn Thr Leu Glu Asp Arg Leu Ala His His Arg Trp Leu
355 360 365
Leu Phe Phe His Phe Gly Lys Asn Glu Asn Ser Asn Asp Pro Glu Leu
370 375 380
Lys Lys Leu Lys Thr Leu Leu Lys Asn Asp His Ile Gln Val Gly Arg
385 390 395 400
Phe Asp Cys Ser Ser Ala Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe
405 410 415
Gln Pro Ser Leu Ala Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu
420 425 430
Ile His His Gly Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys
435 440 445
Glu Ser Val Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro
450 455 460
Ala Asn Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys
465 470 475 480
Pro Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu
485 490 495
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His Glu
500 505 510
Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr Val Val
515 520 525

Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His Ser Ala Glu
530 535 540
Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro Ser Val Val Ser
545 550 555 560
Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr Gln Arg Lys His Asn
565 570 575
Glu Val Trp Met Val Asp Phe Tyr Ser Pro Trp Cys His Pro Cys Gln
580 585 590
Val Leu Met Pro Glu Trp Lys Arg Met Ala Arg Thr Leu Thr Gly Leu
595 600 605
Ile Asn Val Gly Ser Ile Asp Cys Gln Gln Tyr His Ser Phe Cys Ala
610 615 620
Gln Glu Asn Val Gln Arg Tyr Pro Glu Ile Arg Phe Phe Pro Pro Lys
625 630 635 640
Ser Asn Lys Ala Tyr His Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp
645 650 655
Ala Tyr Ser Leu Arg Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser
660 665 670
Thr Asp Leu Thr Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys
675 680 685
Asn His Trp Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln
690 695 700
Asn Phe Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys
705 710 715 720
Val Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln
725 730 735
Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr Glu
740 745 750
Arg Ala Asn Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg Asp Ala
755 760 765
Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr Leu Arg Asn
770 775 780
Gln Gly Lys Arg Asn Lys Asp Glu Leu
785 790

<210> 115
<211> 1286
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (32)..(1171)

<400> 115
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ctactgcgcc aagctctgcg agccgcagtg gttttatgaa gaaacagaaa gcagtgatga 180
tgttgaagtg ctgactctca agaaattcaa aggagacctg gcctacagac gacaagagta 240
tcagaaagca ctgcaggagt attccagtat ctctgaaaaa ttgtcatcaa ccaattttgc 300
catgaaaagg gatgtccagg aaggtcaggc tcggtgtctg gctcacctgg gtaggcatat 360
ggaggcgctg gagattgctg caaacttgga aaataaagca accaacacag accatttaac 420
cacggtactc tacctccagc ttgctatttg ttcaagtttg cagaacttgg agaaaacaat 480
tttctgcctg cagaaactga tttctttgca tccttttaat ccttggaact ggggcaaatt 540
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acagcacagt ttcacctcaa gtgacaaaac tatcaaatcc ttctttccac actcaggaaa 660
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agaagaattt gaagacaagt ggttcagaaa gatcaaagac catttctgtc catttgaaaa 1140
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<210> 116
<211> 380
<212> PRT
<213> Homo sapiens

<400> 116

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             20                  25                  30
Ala Lys Leu Cys Glu Pro Gln Trp Phe Tyr Glu Glu Thr Glu Ser Ser
         35                  40                  45
Asp Asp Val Glu Val Leu Thr Leu Lys Lys Phe Lys Gly Asp Leu Ala
     50                  55                  60
Tyr Arg Arg Gln Glu Tyr Gln Lys Ala Leu Gln Glu Tyr Ser Ser Ile
 65                  70                  75                  80
Ser Glu Lys Leu Ser Ser Thr Asn Phe Ala Met Lys Arg Asp Val Gln
                 85                  90                  95
Glu Gly Gln Ala Arg Cys Leu Ala His Leu Gly Arg His Met Glu Ala
            100                 105                 110
Leu Glu Ile Ala Ala Asn Leu Glu Asn Lys Ala Thr Asn Thr Asp His
        115                 120                 125
Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
    130                 135                 140
Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
145                 150                 155                 160
```

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Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
                165                 170                 175
Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His
            180                 185                 190
Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
        195                 200                 205
Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
    210                 215                 220
Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
225                 230                 235                 240
Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
                245                 250                 255
Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
            260                 265                 270
Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
        275                 280                 285
Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
    290                 295                 300
Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
305                 310                 315                 320
Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
                325                 330                 335
Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
            340                 345                 350
Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe
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Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala
    370                 375                 380
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<210> 117
<211> 1836
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (283)..(732)

<400> 117

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gtcttttgct agtctggact ggagagcaac ttccctgagt caggactctt gctgctaatt 180
gcagaaaacc agcagtctct gtgaagttgt ggtgttctca gagttcagct gtaaaatata 240
gaatcctcat taattgtatt tacaactata ttgagcaaac caatgttgtt ctttattaat 300
gtacagacca aaaaagacac ctcaaaagaa aggacgtacg cgtttcttgt aaacacgagg 360
caccccaaga taagaagaca gatagagcaa gggatggaca tggtcatctc ctcagtgatt 420
ggagaaagtt accggcttca gtttgatttt caagaggcag tgaagaattt cttccccca 480
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ggaaatgaag tggttaatgg agaaaattta agctttgcat atgaattcaa agctgatgca 540
ttatttgatt tcttctattg gtttgggctc agtaattccg ttgtaaaagt aaatggaaaa 600
gttcttttag gttcaataga tgatgttttt aactgcaatc tgtcacccag atcatctctg 660
acagagcctc ttttggcaga attaccattt ccaagtgttc tggaatctga agagacaccc 720
aaccaattta tctgattgaa ctgaacattg tagcagttgc tcccgcactc caggcctgtg 780
ctagactata ggctgggggg agggtaggag gtgggaggca gatacttcca cctgcgtgtc 840
aatctccggc tcctccatgg cttctatgga ggactcctct cttctgcttc tgtggatgtg 900
atgccctggc aggcccaggg cagctgattc ccctaaaact tatgattacc aggatggaaa 960
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ccaagaggca gaagggccac agagttctgc caccctgaac atttttctca gttccctggg 1080
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aaggggttaa gagttctgtt ctcttgccaa cctggctggg caaaagcctg tgccatcttt 1260
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gaacaatgac aggggaaggg tattggacac ggcagcgtcc tccttattga aaacacatta 1500
tgtcagttgg gaattttaaa taagctttta gcaaacctaa cactaaaagc aaaatagaag 1560
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ataatgagga agagttatgg gtcctgagtg taatttttta tcctttctta aaaagtttct 1740
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accacatttg cacaattaaa acttttctta gcattc 1836

<210> 118
<211> 150
<212> PRT
<213> Homo sapiens

<400> 118

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			20					25				30			
Gln	Ile	Glu	Gln	Gly	Met	Asp	Met	Val	Ile	Ser	Ser	Val	Ile	Gly	Glu
		35					40					45			
Ser	Tyr	Arg	Leu	Gln	Phe	Asp	Phe	Gln	Glu	Ala	Val	Lys	Asn	Phe	Phe
	50					55					60				
Pro	Pro	Gly	Asn	Glu	Val	Val	Asn	Gly	Glu	Asn	Leu	Ser	Phe	Ala	Tyr
65					70					75					80
Glu	Phe	Lys	Ala	Asp	Ala	Leu	Phe	Asp	Phe	Phe	Tyr	Trp	Phe	Gly	Leu
				85					90					95	
Ser	Asn	Ser	Val	Val	Lys	Val	Asn	Gly	Lys	Val	Leu	Leu	Gly	Ser	Ile
			100					105				110			
Asp	Asp	Val	Phe	Asn	Cys	Asn	Leu	Ser	Pro	Arg	Ser	Ser	Leu	Thr	Glu
		115					120					125			
Pro	Leu	Leu	Ala	Glu	L u	Pro	Phe	Pro	Ser	Val	Leu	Glu	Ser	Glu	Glu

130 135 140
Thr Pro Asn Gln Phe Ile
145 150

<210> 119
<211> 1863
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (460)..(1233)

<400> 119
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agcgcgttgg gccccgccgg cgatgccgcg cgccgcctcc tcggagcggc ggcgaagttt 180
gaacttggcg tcggcctgga gccccgagca gcccgggggc ggcggccgcg aggcgagcgg 240
cgatgagatg tgtgcacaga cccaggccat gcagatactg gtgcctctaa cttcgtcagc 300
ccttagaaca tgacttgctg tccccagtgg agaagaaacc agaagctaca gccaagtatg 360
tcccctccaa agtccatttc tgttcagtgc ctgaaaatga ggaggatgcc tccctgaaga 420
gacatctcac acctccccaa ggcaacagcc cacattccaa tgagagaaag agcacccccа 480
cctcctccac cgagtcagga aaccccggtg tatagcatgg atgacttccc tccacctcct 540
ccccacactg tatgtgaggc gcagctggac agtgaggatc ccgaggggcc acgccccagc 600
ttcaacaaac tttctaaagt gacaattgca agggaaaggc acatgcctgg tgcagcccat 660
gtggtaggta gtcagacact ggcttccaga ctccaaactt ctatcaaggg ttcagaggct 720
gagtccacac caccctcctt catgagcgtt cacgcccaac ttgctgggtc tcttggtggg 780
cagccagcac ccatccagac tcaaagcctc agccatgatc cagtcagtgg aactcagggt 840
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atggaaaaga tcactatgtt tgttgtgcta accacttatt tgattctgtt ttgtggtgga 1800
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gat 1863

<210> 120
<211> 258
<212> PRT
<213> Homo sapiens

<400> 120

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Val Tyr Ser Met Asp Asp Phe Pro Pro Pro Pro Pro His Thr Val Cys
             20                  25                  30
Glu Ala Gln Leu Asp Ser Glu Asp Pro Glu Gly Pro Arg Pro Ser Phe
         35                  40                  45
Asn Lys Leu Ser Lys Val Thr Ile Ala Arg Glu Arg His Met Pro Gly
     50                  55                  60
Ala Ala His Val Val Gly Ser Gln Thr Leu Ala Ser Arg Leu Gln Thr
 65                  70                  75                  80
Ser Ile Lys Gly Ser Glu Ala Glu Ser Thr Pro Pro Ser Phe Met Ser
                 85                  90                  95
Val His Ala Gln Leu Ala Gly Ser Leu Gly Gly Gln Pro Ala Pro Ile
            100                 105                 110
Gln Thr Gln Ser Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu
        115                 120                 125
Glu Lys Lys Val Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg
    130                 135                 140
Thr Glu Ala Leu Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala
145                 150                 155                 160
Asp Ile Leu Asp Pro Asp Ser Arg Leu Lys Thr Thr Met Asp Leu Met
                165                 170                 175
Glu Gly Leu Phe Pro Arg Asp Val Asn Leu Leu Lys Glu Asn Ser Val
            180                 185                 190
Lys Arg Lys Ala Ile Gln Arg Thr Val Ser Ser Ser Gly Cys Glu Gly
        195                 200                 205
Lys Arg Asn Glu Asp Lys Glu Ala Val Ser Met Leu Val Asn Cys Pro
    210                 215                 220
Gln Ile Ser Phe Pro Arg Leu Gly Pro Trp Leu Cys Pro Gln Thr Ser
225                 230                 235                 240
Arg Val Ser Pro Phe Leu Leu Gly Ala Val Leu Ser Val Val Phe Ser
                245                 250                 255
Gln His
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<210> 121
<211> 2203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(564)

<400> 121
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acaagcctta ggaagttagc tgaacagttc ccacggcaag tcttggacag taaagcacca 480
aaaccagagg acattgatga ggaagatgat gatgttccag atcttgtaga aaattttgat 540
gaggcatcaa agaatgaagc taactaaaag tttggttttt ggaagctggc atggactaga 600
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tacatttgtt acttttcttt tccccccgta agacacagaa ttaatggaaa gtgagtatct 1020
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caaggttgaa attgggaatg tccttttgaa tcagaagaaa ataggccata gactcatctc 1620
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taaggacaaa atttagaaaa tatatcattt cctggcccat catcaaacta atacagctta 1980
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tatatggact aaacaaaata aaataacagt gcaaaagaga aac 2203

<210> 122
<211> 158
<212> PRT
<213> Homo sapiens

<400> 122
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Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg Thr Ala
20 25 30
Thr Ala Asp Asp Lys Lys Leu Gln Ser Ser Leu Lys Lys Leu Ala Val
35 40 45
Asn Asn Ile Ala Gly Ile Glu Glu Val Asn Met Ile Lys Asp Asp Gly
50 55 60
Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ser Ala
65 70 75 80
Asn Thr Phe Ala Ile Thr Gly His Ala Glu Ala Lys Pro Ile Thr Glu
85 90 95
Met Leu Pro Gly Ile Leu Ser Gln Leu Gly Ala Asp Ser Leu Thr Ser
100 105 110
Leu Arg Lys Leu Ala Glu Gln Phe Pro Arg Gln Val Leu Asp Ser Lys
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130 135 140
Leu Val Glu Asn Phe Asp Glu Ala Ser Lys Asn Glu Ala Asn
145 150 155

<210> 123
<211> 1696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (62)..(898)

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<211> 279
<212> PRT
<213> Homo sapiens

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Gly Arg Val Leu Leu Gly Glu Gly Val Leu Thr Lys Glu Cys Arg Lys
35 40 45
Lys Ala Lys Pro Arg Ile Leu Phe Leu Phe Asn Asp Ile Leu Val Tyr
50 55 60
Gly Ser Ile Val Leu Asn Lys Arg Lys Tyr Arg Ser Gln His Ile Ile
65 70 75 80
Pro Leu Glu Glu Val Thr Leu Glu Leu Leu Pro Glu Thr Leu Gln Ala
85 90 95
Lys Asn Arg Trp Met Ile Lys Thr Ala Lys Lys Ser Phe Val Val Ser
100 105 110
Ala Ala Ser Ala Thr Glu Arg Gln Glu Trp Ile Ser His Ile Glu Glu
115 120 125
Cys Val Arg Arg Gln Leu Arg Ala Thr Gly Arg Pro Pro Ser Thr Glu
130 135 140
His Ala Ala Pro Trp Ile Pro Asp Lys Ala Thr Asp Ile Cys Met Arg
145 150 155 160
Cys Thr Gln Thr Arg Phe Ser Ala Leu Thr Arg Arg His His Cys Arg
165 170 175
Lys Cys Gly Phe Val Val Cys Ala Glu Cys Ser Arg Gln Arg Phe Leu
180 185 190
Leu Pro Arg Leu Ser Pro Lys Pro Val Arg Val Cys Ser Leu Cys Tyr

195 200 205
Arg Glu Leu Ala Ala Gln Gln Arg Gln Glu Glu Ala Glu Glu Gln Gly
210 215 220
Ala Gly Ser Pro Gly Gln Pro Ala His Leu Ala Arg Pro Ile Cys Gly
225 230 235 240
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245 250 255
Arg Asp Gly Asp Trp Pro Ser Ser Val Glu Phe Tyr Ala Ser Gly Val
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Ala Trp Ser Ala Phe His Ser
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<211> 3078
<212> DNA
<213> Homo sapiens

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<211> 298
<212> PRT
<213> Homo sapiens

<400> 126
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35 40 45
Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg
50 55 60
Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Lys Arg Lys
65 70 75 80
His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly
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Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys

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145                 150                 155                 160
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Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser Gly Ser Thr Ser Gly Gly
            180                 185                 190
Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg Ser Asp Ser Pro Pro Arg
        195                 200                 205
Gln Ala Pro Arg Ser Ala Pro Tyr Lys Gly Ser Glu Ile Arg Gly Ser
    210                 215                 220
Arg Lys Ser Lys Asp Cys Lys Tyr Pro Gln Lys Pro His Lys Ser Arg
225                 230                 235                 240
Ser Arg Ser Ser Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Ala Asp
                245                 250                 255
Asn Pro Gly Lys Tyr Lys Lys Lys Ser His Tyr Tyr Arg Asp Gln Arg
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<213> Homo sapiens

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<210> 128
<211> 352
<212> PRT
<213> Homo sapiens

<400> 128

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Ala	Glu	Arg	Gly	Lys	Ala	Lys	Asp	Ala	Asp	Leu	Arg	Pro	Gly	Asp	Ile
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Ile	Val	Ala	Ile	Asn	Gly	Glu	Ser	Ala	Glu	Gly	Met	Leu	His	Ala	Glu
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Ala	Gln	Ser	Lys	Ile	Arg	Gln	Ser	Pro	Ser	Pro	Leu	Arg	Leu	Gln	Leu
65					70					75					80
Asp	Arg	Ser	Gln	Ala	Thr	Ser	Pro	Gly	Gln	Thr	Asn	Gly	Asp	Ser	Ser
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Glu	Ser	Gln	Ser	Ser	Leu	Arg	Ser	Ser	Tyr	Ser	Ser	Pro	Thr	Ser	Leu
		115					120					125			
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165 170 175
Gly Ser Arg Gln Ala Gly Leu Gly Arg Ala Gly Asp Ser Ala Val Leu
180 185 190
Val Leu Pro Pro Ser Pro Gly Pro Arg Ser Ser Arg Pro Ser Met Asp
195 200 205
Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser Glu Val Phe Lys
210 215 220
Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro Arg Gln Ser Ser
225 230 235 240
Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu Glu Arg Gly Gly
245 250 255
Thr Pro Ala Phe Leu Pro Ser Ser Leu Ser Pro Gln Ser Ser Leu Pro
260 265 270
Ala Ser Arg Ala Leu Ala Thr Pro Pro Lys Leu His Thr Cys Glu Lys
275 280 285
Cys Ser Thr Ser Ile Ala Asn Gln Ala Val Arg Ile Gln Glu Gly Arg
290 295 300
Tyr Arg His Pro Gly Cys Tyr Thr Cys Ala Asp Cys Gly Leu Asn Leu
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Lys Met Arg Gly His Phe Trp Val Gly Asp Glu Leu Tyr Cys Glu Lys
325 330 335
His Ala Arg Gln Arg Tyr Ser Ala Pro Ala Thr Leu Ser Ser Arg Ala
340 345 350

<210> 129
<211> 2356
<212> DNA
<213> Homo sapiens

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<211> 1731
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (72)..(1373)

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<210> 131
<211> 434
<212> PRT
<213> Homo sapiens

<400> 131
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35 40 45
Glu Glu Lys Glu Lys Tyr Ala Glu Met Ala Arg Glu Trp Arg Ala Ala
50 55 60
Gln Gly Lys Asp Pro Gly Pro Ser Glu Lys Gln Lys Pro Val Phe Thr
65 70 75 80
Pro Leu Arg Arg Pro Gly Met Leu Val Pro Lys Gln Asn Val Ser Pro
85 90 95
Pro Asp Met Ser Ala Leu Ser Leu Lys Gly Asp Gln Ala Leu Leu Gly
100 105 110
Gly Ile Phe Tyr Phe Leu Asn Ile Phe Ser His Gly Glu Leu Pro Pro
115 120 125
His Cys Glu Gln Arg Phe Leu Pro Cys Glu Ile Gly Cys Val Lys Tyr
130 135 140
Ser Leu Gln Glu Gly Ile Met Ala Asp Phe His Ser Phe Ile Asn Pro
145 150 155 160
Gly Glu Ile Pro Arg Gly Phe Arg Phe His Cys Gln Ala Ala Ser Asp
165 170 175
Ser Ser His Lys Ile Pro Ile Ser Asn Phe Glu Arg Gly His Asn Gln

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            180                 185                 190
Ala Thr Val Leu Gln Asn Leu Tyr Arg Phe Ile His Pro Asn Pro Gly
        195                 200                 205
Asn Trp Pro Pro Ile Tyr Cys Lys Ser Asp Asp Arg Thr Arg Val Asn
    210                 215                 220
Trp Cys Leu Lys His Met Ala Lys Ala Ser Glu Ile Arg Gln Asp Leu
225                 230                 235                 240
Gln Leu Leu Thr Val Glu Asp Leu Val Val Gly Ile Tyr Gln Gln Lys
                245                 250                 255
Phe Leu Lys Glu Pro Ser Lys Thr Trp Ile Arg Ser Leu Leu Asp Val
            260                 265                 270
Ala Met Trp Asp Tyr Ser Ser Asn Thr Arg Cys Lys Trp His Glu Glu
        275                 280                 285
Asn Asp Ile Leu Phe Cys Ala Leu Ala Val Cys Lys Lys Ile Ala Tyr
    290                 295                 300
Cys Ile Ser Asn Ser Leu Ala Thr Leu Phe Gly Ile Gln Leu Thr Glu
305                 310                 315                 320
Ala His Val Pro Leu Gln Asp Tyr Glu Ala Ser Asn Ser Val Thr Pro
                325                 330                 335
Lys Met Val Val Leu Asp Ala Gly Arg Tyr Gln Lys Leu Arg Val Gly
            340                 345                 350
Ser Ser Gly Phe Ser His Phe Asn Ser Ser Asn Glu Glu Gln Arg Ser
        355                 360                 365
Asn Thr Pro Ile Gly Asp Tyr Pro Ser Arg Ala Lys Ile Ser Gly Gln
    370                 375                 380
Asn Ser Ser Val Arg Gly Arg Gly Ile Thr Arg Leu Leu Glu Ser Ile
385                 390                 395                 400
Ser Asn Ser Ser Ser Asn Ile His Lys Phe Ser Asn Cys Asp Thr Ser
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Leu Ser Pro Tyr Met Ser Gln Lys Asp Gly Tyr Lys Ser Phe Ser Ser
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Leu Ser
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<210> 132
<211> 1561
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (385)..(1281)

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gcacacaaca ggagagagga gaaagaagaa acgctagtaa ttccaagcac tggaattaag 180

ttgccttcat cagtgtttgc ttcagagttt gaggaagatg ttggattgtt aaataaagca 240
gctccagttt caggacctcg actggatttt gatcctgaca ttgttgcagc tcttgatgat 300
gattttgact ttgatgatcc agataatctg cttgaggatg actttattct tcaggccaat 360
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gagtgggaag atgtggatga tgagaaggga gatagcaatg atgactatga ctctgcaggc 480
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gtcatgagga gaaatgaaca gctgacccta catgatgaga ggtttgagaa gttttatgag 660
caatatgatg atgatgaaat tggagctctg gataatgcag aattggaagg ttctattcaa 720
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gatgagtctg aggaggaaga aatgattact gtagtccttg aagaagccaa agagaagtgg 900
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gcaagaaagc aagctataaa agaagagcgc aaggaacgaa gagtggagaa gaaagctaac 1200
aaattagcat ttaaactgga gaaaagaagg caagaaaaag agctgctgaa cttgaagaag 1260
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gctcctcatc tttggttatt gactagaaac ttcagaaaga caaaactgtt tgccattttt 1380
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t 1561

<210> 133
<211> 299
<212> PRT
<213> Homo sapiens

<400> 133

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Val	Asp	Asp	Glu	Lys	Gly	Asp	Ser	Asn	Asp	Asp	Tyr	Asp	Ser	Ala	Gly
			20					25				30			
Leu	Leu	Ser	Asp	Glu	Asp	Cys	Met	Ser	Val	Pro	Gly	Lys	Thr	His	Arg
		35					40				45				
Ala	Ile	Ala	Asp	His	Leu	Phe	Trp	Ser	Glu	Glu	Thr	Lys	Ser	Arg	Phe
	50					55					60				
Thr	Glu	Tyr	Ser	Met	Thr	Ser	Ser	Val	Met	Arg	Arg	Asn	Glu	Gln	Leu
65					70					75					80
Thr	Leu	His	Asp	Glu	Arg	Phe	Glu	Lys	Phe	Tyr	Glu	Gln	Tyr	Asp	Asp
				85					90					95	
Asp	Glu	Ile	Gly	Ala	Leu	Asp	Asn	Ala	Glu	Leu	Glu	Gly	Ser	Ile	Gln
			100					105					110		
Val	Asp	Ser	Asn	Arg	Leu	Gln	Glu	Val	Leu	Asn	Asp	Tyr	Tyr	Lys	Glu
		115					120					125			

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Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
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Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
145                 150                 155                 160
Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
                165                 170                 175
Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
            180                 185                 190
Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
        195                 200                 205
Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
    210                 215                 220
Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
225                 230                 235                 240
Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
                245                 250                 255
Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
            260                 265                 270
Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
        275                 280                 285
Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu
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<210> 134
<211> 2497
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (305)..(970)

<400> 134

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tgtggtggtg caggagctca agtccatggt ggccaccaag atcgccaaat atgctgtgcc 780
tgatgagatc ctggtggtga aacgtcttcc aaaaaccagg tctgggaagg tcatgcggcg 840
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<210> 135
<211> 222
<212> PRT
<213> Homo sapiens

<400> 135
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Lys Gly Ser Val Val Glu Gly Ser Asn Val Ser Gly Ala Leu Cys Ile
20 25 30
Ser Gln Ala Trp Pro Gly Met Ala Arg Thr Ile Tyr Gly Asp His Gln
35 40 45
Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr Tyr Phe Thr
50 55 60
Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln Ile Thr Gly
65 70 75 80
Arg Met Asp Asp Val Ile Asn Ile Ser Gly His Arg Leu Gly Thr Ala
85 90 95

Glu Ile Glu Asp Ala Ile Ala Asp His Pro Ala Val Pro Glu Ser Ala
100 105 110
Val Ile Gly Tyr Pro His Asp Ile Lys Gly Glu Ala Ala Phe Ala Phe
115 120 125
Ile Val Val Lys Asp Ser Ala Gly Asp Ser Asp Val Val Val Gln Glu
130 135 140
Leu Lys Ser Met Val Ala Thr Lys Ile Ala Lys Tyr Ala Val Pro Asp
145 150 155 160
Glu Ile Leu Val Val Lys Arg Leu Pro Lys Thr Arg Ser Gly Lys Val
165 170 175
Met Arg Arg Leu Leu Arg Lys Ile Ile Thr Ser Glu Ala Gln Glu Leu
180 185 190
Gly Asp Thr Thr Thr Leu Glu Asp Pro Ser Ile Ile Ala Glu Ile Leu
195 200 205
Ser Val Tyr Gln Lys Cys Lys Asp Lys Gln Ala Ala Ala Lys
210 215 220

<210> 136
<211> 1972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (666)..(1487)

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<210> 137
<211> 274
<212> PRT
<213> Homo sapiens

<400> 137

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			20					25					30		
Val	Leu	Phe	Leu	Ser	Lys	Gly	Ser	Ser	Arg	Ala	His	Ile	Pro	Ala	Pro
		35					40					45			
Leu	Glu	Gln	Gly	Val	Val	Ala	Ala	Phe	Lys	Gln	Leu	Tyr	Lys	Arg	Glu
	50					55					60				
Leu	Leu	Arg	Leu	Ala	Val	Ser	Cys	Ala	Ser	Gly	Ser	Pro	Leu	Gly	Phe
65					70					75					80
Met	Arg	Ser	Phe	Met	Leu	Lys	Asp	Met	Leu	Tyr	Leu	Ala	Gly	Leu	Ser
				85					90					95	
Trp	Asp	Leu	Val	Gln	Ala	Gly	Ser	Ile	Glu	Arg	Cys	Trp	Leu	Leu	Gly
			100					105					110		
Leu	Arg	Ala	Ala	Phe	Glu	Pro	Arg	Pro	Gly	Glu	Asp	Ser	Ala	Gly	Gln
		115					120					125			
Pro	Ala	Gln	Ala	Glu	Glu	Ala	Ala	Glu	His	Ser	Arg	Val	Leu	Ser	Asp
	130					135					140				
Leu	Thr	His	Leu	Ala	Ala	Leu	Ala	Tyr	Lys	Cys	Leu	Ala	Pro	Glu	Glu
145					150					155					160
Val	Ala	Glu	Trp	Leu	His	Leu	Asp	Asp	Asp	Gly	Gly	Pro	Pro	Glu	Gly
				165					170					175	
Cys	Arg	Glu	Glu	Val	Gly	Pro	Ala	Leu	Pro	Pro	Ala	Ala	Pro	Pro	Ala
			180					185					190		
Pro	Ala	Ser	Leu	Pro	Ser	Ala	Ile	Gly	Gly	Gly	Glu	Asp	Glu	Glu	Glu
		195					200					205			
Ala	Thr	Asp	Tyr	Gly	Gly	Thr	Ser	Val	Pro	Thr	Ala	Gly	Glu	Ala	Val

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    210                 215                 220
Arg Gly Leu Glu Thr Ala Leu Arg Trp Leu Glu Asn Gln Asp Pro Arg
225                 230                 235                 240
Glu Val Gly Pro Leu Arg Leu Val Gln Leu Arg Ser Leu Ile Ser Met
                245                 250                 255
Ala Arg Arg Leu Gly Gly Ile Gly His Thr Pro Ala Gly Pro Tyr Asp
            260                 265                 270
Gly Val
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<210> 138
<211> 3677
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (996)..(3437)

<400> 138
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<212> PRT
<213> Homo sapiens

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Gln Ala Trp Ser Arg Phe Ser Phe Glu Ile Glu Ala Arg Ala Gln Glu
                 85                  90                  95
Asn Ala Asp Ala Ser Thr Asn Val Asn Phe Ser Arg Gly Ala Ser Thr
            100                 105                 110
Arg Ala Gly Phe Ser Asp Gly Ala Ser Ile Ser Phe Asn Gly Ala Pro
        115                 120                 125
Ser Ser Ser Gly Gly Phe Ser Gly Gly Pro Gly Ile Thr Phe Gly Val
    130                 135                 140
Ala Pro Ser Thr Ser Ala Ser Phe Ser Asn Thr Ala Ser Ile Ser Phe
145                 150                 155                 160
Gly Gly Thr Leu Ser Thr Ser Ser Ser Phe Ser Ser Ala Ala Ser Ile
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Ser Phe Gly Cys Ala His Ser Thr Ser Thr Ser Phe Ser Ser Glu Ala
            180                 185                 190
Ser Ile Ser Phe Gly Gly Met Pro Cys Thr Ser Ala Ser Phe Ser Gly
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225                 230                 235                 240
Gly Phe Ser Gly Val Leu Ser Thr Ser Thr Ser Phe Gly Ser Ala Pro
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Thr Thr Ser Thr Val Phe Ser Ser Ala Leu Ser Thr Ser Thr Gly Phe
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Gly Gly Ile Leu Ser Thr Ser Val Cys Phe Gly Gly Ser Pro Ser Ser
        275                 280                 285
Ser Gly Ser Phe Gly Gly Thr Leu Ser Thr Ser Ile Cys Phe Gly Gly
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Ser Pro Cys Thr Ser Thr Gly Phe Gly Gly Thr Leu Ser Thr Ser Val
305                 310                 315                 320
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545                 550                 555                 560
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Ser Ala Gly Phe Ser Gly Gly Leu Ser Thr Ser Asp Gly Phe Gly Ser
    690                 695                 700
Arg Pro Asn Ala Ser Phe Asp Arg Gly Leu Ser Thr Ile Ile Gly Phe
705                 710                 715                 720
Gly Ser Gly Ser Asn Thr Ser Thr Gly Phe Thr Gly Glu Pro Ser Thr
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Ser Thr Gly Phe Ser Ser Gly Pro Ser Ser Ile Val Gly Phe Ser Gly
            740                 745                 750
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        755                 760                 765
Phe Ser Gly Gly Pro Ser Thr Gly Ala Gly Phe Gly Gly Gly Pro Asn
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<212> DNA
<213> Homo sapiens

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<222> (72)..(1910)

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<212> PRT
<213> Homo sapiens

<400> 141

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        35                  40                  45
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    50                  55                  60
Pro Ala Thr Leu Val Ile Ile Ile Phe Ile Cys Phe Gln Gln Lys Ser
65                  70                  75                  80
Tyr Val Ser Ser Thr Asn Leu Pro Val Leu Ala Leu Leu Leu Leu Leu
                85                  90                  95
Tyr Gly Trp Ser Ile Thr Pro Leu Met Tyr Pro Ala Ser Phe Val Phe
            100                 105                 110
Lys Ile Pro Ser Thr Ala Tyr Val Val Leu Thr Ser Val Asn Leu Phe
        115                 120                 125
Ile Gly Ile Asn Gly Ser Val Ala Thr Phe Val Leu Glu Leu Phe Thr
    130                 135                 140
Asp Asn Lys Leu Asn Asn Ile Asn Asp Ile Leu Lys Ser Val Phe Leu
145                 150                 155                 160
Ile Phe Pro His Phe Cys Leu Gly Arg Gly Leu Ile Asp Met Val Lys
                165                 170                 175
Asn Gln Ala Met Ala Asp Ala Leu Glu Arg Phe Gly Glu Asn Arg Phe
            180                 185                 190
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        195                 200                 205
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Arg Phe Phe Ile Arg Pro Arg Pro Val Asn Ala Lys Leu Ser Pro Leu
225                 230                 235                 240
Asn Asp Glu Asp Glu Asp Val Arg Arg Glu Arg Gln Arg Ile Leu Asp
                245                 250                 255
Gly Gly Gly Gln Asn Asp Ile Leu Glu Ile Lys Glu Leu Thr Lys Ile
            260                 265                 270
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        275                 280                 285
Pro Pro Gly Glu Cys Phe Gly Leu Leu Gly Val Asn Gly Ala Gly Lys
    290                 295                 300
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Asp Ala Phe Leu Asn Lys Asn Ser Ile Leu Ser Asn Ile His Glu Val
325 330 335
His Gln Asn Met Gly Tyr Cys Pro Gln Phe Asp Ala Ile Thr Glu Leu
340 345 350
Leu Thr Gly Arg Glu His Val Glu Phe Phe Ala Leu Leu Arg Gly Val
355 360 365
Pro Glu Lys Glu Val Gly Lys Val Gly Glu Trp Ala Ile Arg Lys Leu
370 375 380
Gly Leu Val Lys Tyr Gly Glu Lys Tyr Ala Gly Asn Tyr Ser Gly Gly
385 390 395 400
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405 410 415
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420 425 430
Arg Phe Leu Trp Asn Cys Ala Leu Ser Val Val Lys Glu Gly Arg Ser
435 440 445
Val Val Leu Thr Ser His Ser Met Glu Glu Cys Glu Ala Leu Cys Thr
450 455 460
Arg Met Ala Ile Met Val Asn Gly Arg Phe Arg Cys Leu Gly Ser Val
465 470 475 480
Gln His Leu Lys Asn Arg Phe Gly Asp Gly Tyr Thr Ile Val Val Arg
485 490 495
Ile Ala Gly Ser Asn Pro Asp Leu Lys Pro Val Gln Asp Phe Phe Gly
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Leu Ala Phe Pro Gly Ser Val Leu Lys Glu Lys His Arg Asn Met Leu
515 520 525
Gln Tyr Gln Leu Pro Ser Ser Leu Ser Ser Leu Ala Arg Ile Phe Ser
530 535 540
Ile Leu Ser Gln Ser Lys Lys Arg Leu His Ile Glu Asp Tyr Ser Val
545 550 555 560
Ser Gln Thr Thr Leu Asp Gln Val Phe Val Asn Phe Ala Lys Asp Gln
565 570 575
Ser Asp Asp Asp His Leu Lys Asp Leu Ser Leu His Lys Asn Gln Thr
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<222> (81)..(734)

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35 40 45
Glu Gln Met Leu Arg Lys Asp Gln Lys Thr Ile Tyr Arg Gln Gly Val
50 55 60
Lys Val Ala Ile Ser Ala Ile Tyr Met Asp Leu Glu Ile Cys Glu Val
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Leu Glu Arg Ser His Ser Pro Pro Leu Lys Leu Thr Pro Ala Ser Ser
85 90 95
Thr His Pro Asn Leu His Ala Tyr Leu Gln Gly Asn Thr Gln Val Ser
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Arg Lys Lys Leu Leu Pro Leu Leu Gln Glu Ala Leu Ser Ala Tyr Phe
115 120 125
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130 135 140
Arg Glu Gln Val Asp Lys Glu Leu Asp Arg Ala Ser Asn Ser Leu Ile
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Ser Gly Leu Ser Gln Asp Glu Glu Asp Pro Pro Leu Pro Pro Thr Pro
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Met Asn Ser Leu Val Asp Glu Cys Pro Leu Asp Gln Gly Leu Pro Lys
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35 40 45
Ser Tyr Val Ser Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val
50 55 60
Val Thr Leu Trp Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro
65 70 75 80
Ile Arg Val Val Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala
85 90 95
Ser Leu Trp His His Val Ala Pro Val Ala Gly Gln Leu His Ser Val
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Ala Ser Thr Phe Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala
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Ala Ala Phe Gln Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val
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Pro Thr Gly Glu Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala
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Tyr Gly Arg Leu Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala
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35 40 45
Asn Asp Ser Asp Asp Asp Asp Glu Ala Glu Asp Asp Asp Glu Thr Glu
50 55 60
Glu Leu Gly Ser Asp Glu Asp Asp Ile Asp Glu Asp Gly Gln Glu Tyr
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85 90 95
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Ile Ile Asp Asp Glu Asp Asn Pro Val Asp Glu Tyr Gln Ile Phe Lys
115 120 125
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<212> DNA
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<212> PRT
<213> Homo sapiens

<400> 149

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     50                  55                  60
Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
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Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Leu Gly
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Asn Arg Leu Cys Ala Ser Ile His Phe Ser Ser Ser Thr Trp Val Thr
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Gly Asp Pro Phe Ile Ile Ile His Ser Ile Ser Leu Leu Asn Ala Glu
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Glu His Ser Ile Ala Thr Leu Leu Leu Arg Ile Glu Lys Glu Glu Leu
180 185 190
Asp Met Lys Gly Ser Gly Phe Tyr Val Ser Leu Glu Trp Val Thr Ile
195 200 205
Ser Lys Lys Asn Gln Asp Asn Lys Lys Tyr Glu Ile Ile Lys Arg Asp
210 215 220
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Gly Asn Gly Leu Met Ile Val Ser Tyr Lys Ser Leu Thr Phe Val Gln
245 250 255
Ala Gly Gln Asp Leu Glu Glu Asn Met Asp Glu Asp Ile Ser Glu Lys
260 265 270
Ile Lys Glu Pro Leu Tyr Tyr Trp Gln Gln Thr Glu Asp Asp Leu Thr
275 280 285
Val Thr Ile Arg Leu Pro Glu Asp Ser Thr Lys Glu Asp Ile Gln Ile
290 295 300
Gln Phe Leu Pro Asp His Ile Asn Ile Val Leu Lys Asp His Gln Phe
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Leu Glu Gly Lys Leu Tyr Ser Ser Ile Asp His Glu Ser Ser Thr Trp
325 330 335
Ile Ile Lys Glu Ser Asn Ser Leu Glu Ile Ser Leu Ile Lys Lys Asn
340 345 350
Glu Gly Leu Thr Trp Pro Glu Leu Val Ile Gly Asp Lys Gln Gly Glu
355 360 365
Leu Ile Arg Asp Ser Ala Gln Cys Ala Ala Ile Ala Glu Arg Leu Met
370 375 380
His Leu Thr Ser Glu Glu Leu Asn Pro Asn Pro Asp Lys Glu Lys Pro
385 390 395 400
Pro Cys Ser Ala Gln Glu Leu Glu Glu Cys Asp Ile Phe Phe Glu Glu
405 410 415
Ser Ser Ser Leu Cys Arg Phe Asp Gly Asn Thr Leu Lys Thr Thr His
420 425 430
Val Val Asn Leu Gly Ser Asn Gln Tyr Leu Phe Ser Val Ile Val Asp
435 440 445
Pro Lys Glu Met Pro Cys Phe Cys Leu Arg His Asp Val Asp Ala Leu
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Leu Trp Gln Pro His Ser Ser Lys Gln Asp Asp Met Trp Glu His Ile
465 470 475 480

Ala Thr Phe Asn Ala Leu Gly Tyr Val Gln Ala Ser Lys Arg Asp Lys
485 490 495
Lys Phe Phe Ala Cys Ala Pro Asn Tyr Ser Tyr Ala Ala Leu Cys Glu
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Cys Leu Arg Arg Val Phe Ile Tyr Arg Gln Pro Ala Pro Met Ser Thr
515 520 525
Val Leu Tyr Asn Arg Lys Glu Gly Arg Gln Val Gly Gln Val Ala Lys
530 535 540
Gln Gln Val Ala Ser Leu Glu Thr Asn Asp Pro Ile Leu Gly Phe Gln
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<210> 156
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<220>
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<400> 156
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<210> 157
<211> 17
<212> DNA
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<220>
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caggaaacag ctatgac 17

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP00/05063

A. CLASSIFICATION OF SUBJECT MATTER
Int.Cl[7] C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int.Cl[7] C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq, MEDLINE (STN)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 98/37094, A2 (GENETICS INST.INC.), 27 August, 1998 (27.08.98) & AU, 9863373, A & EP, 971950, A2	1-13
P,X	WO, 99/55858, A2 (METAGEN GES.GENOMFORSCHUNG MBH), 04 November, 1999 (04.11.99) & DE, 19820190, A1	1-13
P,X	SUZUKI Y. et al., "Statistical analysis of the 5' untranslated region of human mRNA using "Oligo-Capped" cDNA libraries", Genomics (March 2000) Vol.64, No.3, pp.286-297	1-13

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
19 October, 2000 (19.10.00)	31 October, 2000 (31.10.00)
Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
Facsimile No.	Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP00/05063

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The inventions as set forth in claims 1 to 13 are classified into 75 groups of inventions, i.e., inventions relating to DNA containing the base sequences represented in SEQ ID NOS : 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 130, 132, 134, 136, 138, 140, 142, 144, 146 and 148 (each corresponding to a part of claims 1 to 13) and these groups of inventions are not considered as relating to a group of inventions so linked as to form a single general inventive concept.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Inventions relating to DNA containing the base s quence represented by SEQ ID NO:1 as set forth in claims 1 to 13.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

国際調査報告

国際出願番号　PCT／JP00／05063

A.　発明の属する分野の分類（国際特許分類（IPC））

Int.Cl' C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

B.　調査を行った分野

調査を行った最小限資料（国際特許分類（IPC））

Int.Cl' C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース（データベースの名称、調査に使用した用語）

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq, MEDLINE(STN)

C.　関連すると認められる文献

引用文献のカテゴリー＊	引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示	関連する請求の範囲の番号
X	WO, 98/37094, A2 (GENETICS INST. INC.) 27.8月.1998(27.08.98) & AU, 9863373, A & EP, 971950, A2	1-13
P, X	WO, 99/55858, A2 (METAGEN GES. GENOMFORSCHUNG MBH) 4.11月.1999 (04.11.99) & DE, 19820190, A1	1-13
P, X	SUZUKI, Y. et al. "Statistical analysis of the 5' untranslated region of human mRNA using "Oligo-Capped" cDNA libraries", Genomics (2000. Mar.) Vol. 64, No. 3, p. 286-297	1-13

☐ C欄の続きにも文献が列挙されている。　☐ パテントファミリーに関する別紙を参照。

＊　引用文献のカテゴリー
「A」特に関連のある文献ではなく、一般的技術水準を示すもの
「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献（理由を付す）
「O」口頭による開示、使用、展示等に言及する文献
「P」国際出願日前で、かつ優先権の主張の基礎となる出願の日の後に公表された文献
「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「&」同一パテントファミリー文献

国際調査を完了した日　19.10.00	国際調査報告の発送日　31.10.00
国際調査機関の名称及びあて先 日本国特許庁（ISA／JP） 郵便番号100－8915 東京都千代田区霞が関三丁目4番3号	特許庁審査官（権限のある職員）　4B　9281 高堀　栄二 電話番号　03－3581－1101　内線　3448

様式PCT／ISA／210（第2ページ）（1998年7月）

国際調査報告

国際出願番号　ＰＣＴ／ＪＰ００／０５０６３

第Ⅰ欄　請求の範囲の一部の調査ができないときの意見（第１ページの２の続き）

法第８条第３項（ＰＣＴ１７条(2)(a)）の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☐ 請求の範囲 _____ は、この国際調査機関が調査をすることを要しない対象に係るものである。
つまり、

2. ☐ 請求の範囲 _____ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、

3. ☐ 請求の範囲 _____ は、従属請求の範囲であってＰＣＴ規則6.4(a)の第２文及び第３文の規定に従って記載されていない。

第Ⅱ欄　発明の単一性が欠如しているときの意見（第１ページの３の続き）

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

請求の範囲１－１３に記載された発明は、配列番号１、３、５、７、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８に記載の塩基配列を含むＤＮＡに係る発明群（それぞれ請求の範囲１－１３の一部）の７５の発明群に区分され、当該発明群が単一の一般的発明概念を形成するように連関している一群の発明であるとは認められない。

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。

2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。

3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。

4. ☒ 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

請求の範囲１－１３の配列番号１に記載の塩基配列を含むＤＮＡに係る発明

追加調査手数料の異議の申立てに関する注意

☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。

☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。